

Seq. No.	232017
Seq. ID	LIB3197-045-Q1-M1-B1
Method	BLASTX
NCBI GI	g4512667
BLAST score	383
E value	4.0e-37
Match length	109
% identity	69
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

```
Seq. No.          232018
Seq. ID           LIB3197-045-Q1-M1-B10
Method            BLASTX
NCBI GI           g4508079
BLAST score       348
E value           7.0e-33
Match length      110
% identity        62
NCBI Description   (AC005882) 66284 [Arabidopsis thaliana]
```

```
Seq. No.      232019
Seq. ID      LIB3197-045-Q1-M1-B11
Method      BLASTX
NCBI GI      g266944
BLAST score   597
E value      3.0e-62
Match length  117
% identity    95
NCBI Description  60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
>gi_71078_pir_R5TOL8 ribosomal protein L8, cytosolic -
tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein
L2 [Lycopersicon esculentum]
```

Seq. No.	232020
Seq. ID	LIB3197-045-Q1-M1-B12
Method	BLASTX
NCBI GI	g2791834
BLAST score	756
E value	1.0e-80
Match length	143
% identity	99
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	232021
Seq. ID	LIB3197-045-Q1-M1-B2
Method	BLASTX
NCBI GI	g2829870
BLAST score	453
E value	3.0e-45
Match length	135
% identity	65
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

```
Seq. No.      232022
Seq. ID      LIB3197-045-Q1-M1-B3
Method       BLASTX
```


Method BLASTX
 NCBI GI g464707
 BLAST score 530
 E value 3.0e-54
 Match length 109
 % identity 94
 NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana
 >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana]
 >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana]
 >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana]
 >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. 232028
 Seq. ID LIB3197-045-Q1-M1-C12
 Method BLASTX
 NCBI GI g2811278
 BLAST score 638
 E value 7.0e-67
 Match length 130
 % identity 88
 NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 232029
 Seq. ID LIB3197-045-Q1-M1-C5
 Method BLASTX
 NCBI GI g3913414
 BLAST score 287
 E value 7.0e-51
 Match length 142
 % identity 75
 NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 2 (ADOMETDC 2) (SAMDC 2) (SAMDC16) >gi_1155242 (U38527) S-adenosylmethionine decarboxylase 2 [Dianthus caryophyllus]

Seq. No. 232030
 Seq. ID LIB3197-045-Q1-M1-C7
 Method BLASTX
 NCBI GI g2967452
 BLAST score 157
 E value 5.0e-11
 Match length 84
 % identity 42
 NCBI Description (AB010882) hSNF2H [Homo sapiens]
 >gi_4507075_ref_NP_003592.1_pSMARCA5_SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member

[Actinidia deliciosa]

Seq. No. 232045
Seq. ID LIB3197-045-Q1-M1-E9
Method BLASTX
NCBI GI g2499612
BLAST score 432
E value 5.0e-51
Match length 138
% identity 76
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (PMEK1)
>gi_1076650_pir_S52989 mitogen-activated,
extracellular-regulated protein kinase 1 (EC 2.7.1.-) -
garden petunia >gi_603871_emb_CAA58466_ (X83440) MAP/ERK
kinase_1 [Petunia x hybrida]

Seq. No. 232046
Seq. ID LIB3197-045-Q1-M1-F1
Method BLASTX
NCBI GI g2286153
BLAST score 402
E value 2.0e-39
Match length 83
% identity 96
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 232047
Seq. ID LIB3197-045-Q1-M1-F10
Method BLASTX
NCBI GI g4138137
BLAST score 566
E value 2.0e-58
Match length 134
% identity 71
NCBI Description (AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No. 232048
Seq. ID LIB3197-045-Q1-M1-F11
Method BLASTX
NCBI GI g126896
BLAST score 611
E value 9.0e-64
Match length 132
% identity 90
NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
>gi_319831_pir_DEPUMW malate dehydrogenase (EC 1.1.1.37)
precursor, mitochondrial - watermelon
>gi_18297_emb_CAA35239_ (X17362) precursor protein (AA 27
to 320) [Citrullus lanatus]

Seq. No. 232049
Seq. ID LIB3197-045-Q1-M1-F12
Method BLASTX
NCBI GI g2499607
BLAST score 719
E value 2.0e-76
Match length 139

% identity	94
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 3 (MAP KINASE 3) (ATMPK3) >gi_629544_pir_S40469 mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457398_dbj_BAA04866_ (D21839) MAP kinase [Arabidopsis thaliana]
Seq. No.	232050
Seq. ID	LIB3197-045-Q1-M1-F2
Method	BLASTX
NCBI GI	g3650378
BLAST score	156
E value	2.0e-10
Match length	56
% identity	52
NCBI Description	(AL031740) putative rRNA biogenesis protein; rrp5 homolog; multiple S1 rna binding domain protein [Schizosaccharomyces pombe]
Seq. No.	232051
Seq. ID	LIB3197-045-Q1-M1-F4
Method	BLASTX
NCBI GI	g3493172
BLAST score	623
E value	4.0e-65
Match length	133
% identity	92
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]
Seq. No.	232052
Seq. ID	LIB3197-045-Q1-M1-F5
Method	BLASTX
NCBI GI	g2245378
BLAST score	679
E value	1.0e-71
Match length	139
% identity	88
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]
Seq. No.	232053
Seq. ID	LIB3197-045-Q1-M1-F6
Method	BLASTX
NCBI GI	g125887
BLAST score	223
E value	3.0e-18
Match length	115
% identity	44
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir_S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]
Seq. No.	232054
Seq. ID	LIB3197-045-Q1-M1-F7
Method	BLASTX
NCBI GI	g3334115
BLAST score	457

E value 9.0e-46
 Match length 97
 % identity 93
 NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No. 232055
 Seq. ID LIB3197-045-Q1-M1-F8
 Method BLASTX
 NCBI GI g3080420
 BLAST score 497
 E value 2.0e-50
 Match length 121
 % identity 75
 NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No. 232056
 Seq. ID LIB3197-045-Q1-M1-F9
 Method BLASTX
 NCBI GI g870726
 BLAST score 427
 E value 4.0e-42
 Match length 116
 % identity 76
 NCBI Description (L38260) biotin carboxylase subunit [Nicotiana tabacum] >gi_1582354_prf_2118337A Ac-CoA carboxylase:SUBUNIT=biotin carboxylase [Nicotiana tabacum]

Seq. No. 232057
 Seq. ID LIB3197-045-Q1-M1-G3
 Method BLASTX
 NCBI GI g1946355
 BLAST score 358
 E value 4.0e-34
 Match length 124
 % identity 56
 NCBI Description (U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 232058
 Seq. ID LIB3197-045-Q1-M1-G4
 Method BLASTX
 NCBI GI g4544409
 BLAST score 404
 E value 2.0e-39
 Match length 123
 % identity 63
 NCBI Description (AC006955) putative transcription factor [Arabidopsis thaliana]

Seq. No. 232059
 Seq. ID LIB3197-045-Q1-M1-G6
 Method BLASTX

NCBI GI g2129578
 BLAST score 224
 E value 1.0e-33
 Match length 139
 % identity 62
 NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf_2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No. 232060
 Seq. ID LIB3197-045-Q1-M1-G8
 Method BLASTX
 NCBI GI g3242705
 BLAST score 354
 E value 1.0e-33
 Match length 82
 % identity 77
 NCBI Description (AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No. 232061
 Seq. ID LIB3197-045-Q1-M1-H11
 Method BLASTX
 NCBI GI g1220196
 BLAST score 586
 E value 8.0e-61
 Match length 131
 % identity 85
 NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 232062
 Seq. ID LIB3197-045-Q1-M1-H4
 Method BLASTX
 NCBI GI g4098128
 BLAST score 589
 E value 4.0e-61
 Match length 130
 % identity 88
 NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 232063
 Seq. ID LIB3197-045-Q1-M1-H7
 Method BLASTX
 NCBI GI g1707017
 BLAST score 685
 E value 2.0e-72
 Match length 143
 % identity 92
 NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 232064
 Seq. ID LIB3197-045-Q1-M1-H9
 Method BLASTX
 NCBI GI g3925703
 BLAST score 578

% identity	56
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.	232070
Seq. ID	LIB3197-046-Q1-M1-B1
Method	BLASTX
NCBI GI	g3128234
BLAST score	338
E value	1.0e-31
Match length	110
% identity	66
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]
Seq. No.	232071
Seq. ID	LIB3197-046-Q1-M1-B11
Method	BLASTX
NCBI GI	g4056494
BLAST score	368
E value	3.0e-35
Match length	88
% identity	76
NCBI Description	(AC005896) putative protein translocase [Arabidopsis thaliana]
Seq. No.	232072
Seq. ID	LIB3197-046-Q1-M1-B12
Method	BLASTX
NCBI GI	g4193388
BLAST score	489
E value	3.0e-56
Match length	137
% identity	83
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]
Seq. No.	232073
Seq. ID	LIB3197-046-Q1-M1-B4
Method	BLASTX
NCBI GI	g2497753
BLAST score	185
E value	4.0e-14
Match length	48
% identity	62
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]
Seq. No.	232074
Seq. ID	LIB3197-046-Q1-M1-B6
Method	BLASTX
NCBI GI	g728880
BLAST score	443
E value	4.0e-46
Match length	139
% identity	69
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase

Match length	137
% identity	80
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.	232091
Seq. ID	LIB3197-046-Q1-M1-F12
Method	BLASTX
NCBI GI	g1362152
BLAST score	238
E value	5.0e-20
Match length	85
% identity	49
NCBI Description	ribosomal protein S6 kinase homolog (clone Aspk11) - oat >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa]
Seq. No.	232092
Seq. ID	LIB3197-046-Q1-M1-F6
Method	BLASTX
NCBI GI	g2500354
BLAST score	625
E value	2.0e-65
Match length	119
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]
Seq. No.	232093
Seq. ID	LIB3197-046-Q1-M1-F7
Method	BLASTX
NCBI GI	g125051
BLAST score	340
E value	3.0e-32
Match length	83
% identity	81
NCBI Description	ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD) >gi_88038_pir_A37033 isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human >gi_306897 (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens] >gi_4504799_ref_NP_002216.1_pIVD_ isovaleryl Coenzyme A dehydrogenase
Seq. No.	232094
Seq. ID	LIB3197-046-Q1-M1-F8
Method	BLASTX
NCBI GI	g3668089
BLAST score	298
E value	3.0e-27
Match length	104
% identity	51
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	232095
Seq. ID	LIB3197-046-Q1-M1-F9
Method	BLASTX
NCBI GI	g475598
BLAST score	301


```
Seq. No.      232111
Seq. ID       LIB3197-046-Q1-M1-H8
Method        BLASTX
NCBI GI       g3043428
BLAST score    326
E value        2.0e-30
Match length   96
% identity     74
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
```

Seq. No.	232112
Seq. ID	LIB3197-047-Q1-M1-A1
Method	BLASTX
NCBI GI	g3420751
BLAST score	343
E value	2.0e-32
Match length	121
% identity	52
NCBI Description	(AF079448) cytochrome c oxidase assembly protein [Dictyostelium discoideum]

```
Seq. No.      232113
Seq. ID      LIB3197-047-Q1-M1-A10
Method       BLASTX
NCBI GI      g1168972
BLAST score   369
E value      2.0e-35
Match length  115
% identity    42
NCBI Description  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
                PRECURSOR >gi_480969_pir_S37557 clpA protein - rape
                (fragment) >gi_406311_emb_CAA53077_ (X75328) clpA [Brassica
                napus]
```

```
Seq. No.          232114
Seq. ID           LIB3197-047-Q1-M1-A11
Method            BLASTX
NCBI GI           g2160151
BLAST score       362
E value           1.0e-34
Match length      122
% identity        61
NCBI Description  (AC0000375) Strong similarity to Brassica aspartic protease
                  (gb X77260). [Arabidopsis thaliana]
```

```
Seq. No.      232115
Seq. ID       LIB3197-047-Q1-M1-A2
Method        BLASTX
NCBI GI       g1107526
BLAST score   142
E value       1.0e-08
Match length  59
% identity    42
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
```

Seq. No. 232116
Seq. ID LIB3197-047-Q1-M1-A4


```
Seq. No.      232136
Seq. ID      LIB3197-047-Q1-M1-D12
Method       BLASTX
NCBI GI      g119351
BLAST score   203
E value      8.0e-16
Match length  52
% identity    77
NCBI Description  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_84950_pir_S07586
                phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly
                (Drosophila melanogaster) >gi_7946_emb_CAA34895_ (X17034)
                enolase (AA 1-433) [Drosophila melanogaster]
```

```
Seq. No.      232137
Seq. ID      LIB3197-047-Q1-M1-D3
Method       BLASTX
NCBI GI      g135535
BLAST score   300
E value      2.0e-27
Match length  67
% identity   88
NCBI Description  T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
                (CCT-ALPHA) >gi_322602_pir_JN0448 t-complex polypeptide
                Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955
                (D11351) t-complex polypeptide 1 homologue [Arabidopsis
                thaliana] >gi_2326265_dbj_BAA21772 (D11352) CCT
                alpha/TCP-1 [Arabidopsis thaliana]
```

```
Seq. No.      232138
Seq. ID       LIB3197-047-Q1-M1-D5
Method        BLASTX
NCBI GI       g2102696
BLAST score   259
E value       2.0e-22
Match length  128
% identity    38
NCBI Description (U72761) karyopherin beta 3 [Homo sapiens]
               >gi_4504909_ref_NP_002262.1_pKPNB3_ karyopherin (importin)
               beta
```

```

Seq. No.      232139
Seq. ID       LIB3197-047-Q1-M1-D8
Method        BLASTX
NCBI GI       g1169534
BLAST score   645
E value       9.0e-68
Match length  134
% identity    93
NCBI Description  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir_S39203
                phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus
                communis]

```

Seq. No. 232140

BLAST score 303
 E value 1.0e-27
 Match length 118
 % identity 57
 NCBI Description (AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No. 232146
 Seq. ID LIB3197-047-Q1-M1-F8
 Method BLASTX
 NCBI GI g586076
 BLAST score 615
 E value 2.0e-64
 Match length 115
 % identity 97
 NCBI Description TUBULIN BETA-1 CHAIN >gi_486734_pir_S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No. 232147
 Seq. ID LIB3197-047-Q1-M1-F9
 Method BLASTX
 NCBI GI g2431769
 BLAST score 233
 E value 1.0e-23
 Match length 78
 % identity 78
 NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]

Seq. No. 232148
 Seq. ID LIB3197-047-Q1-M1-G1
 Method BLASTX
 NCBI GI g2811278
 BLAST score 651
 E value 2.0e-68
 Match length 133
 % identity 88
 NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 232149
 Seq. ID LIB3197-047-Q1-M1-G10
 Method BLASTX
 NCBI GI g3176387
 BLAST score 473
 E value 1.0e-47
 Match length 99
 % identity 85
 NCBI Description (AB009849) neuropsin [Homo sapiens]

Seq. No. 232150
 Seq. ID LIB3197-047-Q1-M1-G11
 Method BLASTX
 NCBI GI g399082
 BLAST score 148
 E value 2.0e-09
 Match length 112
 % identity 37

NCBI Description ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
>gi_322713_pir_S28171 H+-transporting ATP synthase (EC
3.6.1.34) delta chain, chloroplast - garden pea >gi_169045
(M94558) ATP synthase delta subunit [Pisum sativum]

Seq. No. 232151
Seq. ID LIB3197-047-Q1-M1-G2
Method BLASTX
NCBI GI g2736147
BLAST score 446
E value 2.0e-44
Match length 104
% identity 75
NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis
thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase,
FAH1 [Arabidopsis thaliana]

Seq. No. 232152
Seq. ID LIB3197-047-Q1-M1-G3
Method BLASTX
NCBI GI g3355486
BLAST score 315
E value 4.0e-29
Match length 102
% identity 62
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 232153
Seq. ID LIB3197-047-Q1-M1-G5
Method BLASTX
NCBI GI g3775987
BLAST score 497
E value 2.0e-50
Match length 118
% identity 86
NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No. 232154
Seq. ID LIB3197-047-Q1-M1-G6
Method BLASTX
NCBI GI g2213884
BLAST score 416
E value 5.0e-45
Match length 137
% identity 70
NCBI Description (AF004166) 2-isopropylmalate synthase [Lycopersicon
pennellii]

Seq. No. 232155
Seq. ID LIB3197-047-Q1-M1-G8
Method BLASTX
NCBI GI g3024127
BLAST score 481
E value 1.0e-48
Match length 95
% identity 96
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

D E B I T O R S

Match length 102
 % identity 67
 NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir_JN0718
 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
 precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
 (D13042) thiol protease [Arabidopsis thaliana]
 >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
 cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 232167
 Seq. ID LIB3197-048-Q1-M1-B10
 Method BLASTX
 NCBI GI g4539324
 BLAST score 205
 E value 4.0e-19
 Match length 134
 % identity 46
 NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 232168
 Seq. ID LIB3197-048-Q1-M1-B11
 Method BLASTX
 NCBI GI g1155261
 BLAST score 347
 E value 8.0e-33
 Match length 95
 % identity 74
 NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis
 thaliana]

Seq. No. 232169
 Seq. ID LIB3197-048-Q1-M1-B4
 Method BLASTX
 NCBI GI g2961300
 BLAST score 517
 E value 1.0e-52
 Match length 107
 % identity 93
 NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No. 232170
 Seq. ID LIB3197-048-Q1-M1-B5
 Method BLASTX
 NCBI GI g3914097
 BLAST score 191
 E value 1.0e-14
 Match length 68
 % identity 60
 NCBI Description MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP) (INOSITOL
 MONOPHOSPHATASE) >gi_2708322 (AF037220) inositol
 monophosphatase [Mesembryanthemum crystallinum]

Seq. No. 232171
 Seq. ID LIB3197-048-Q1-M1-B6
 Method BLASTX
 NCBI GI g3522929
 BLAST score 708


```
E value          4.0e-75
Match length     142
% identity       92
NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase
                  [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
```

```

Seq. No.          232172
Seq. ID           LIB3197-048-Q1-M1-C10
Method            BLASTX
NCBI GI           gl20649
BLAST score       444
E value           8.0e-54
Match length      140
% identity        79
NCBI Description  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
                  >gi_625203_pir_DEHUG3 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851)
                  glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]
                  >gi_182863 (J02642) glyceraldehyde 3-phosphate
                  dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977
                  (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC
                  1.2.1.12) [Homo sapiens] >gi_182981 (J04038)
                  glyceraldehyde-3-phosphate dehydrogenase [Homo. sapiens]
                  >gi_224880_prf_1203217A
                  dehydrogenase, glyceraldehydophosphate [Homo sapiens]

```

```
Seq. No.      232173
Seq. ID       LIB3197-048-Q1-M1-C11
Method        BLASTX
NCBI GI       g2651303
BLAST score    230
E value       5.0e-19
Match length   101
% identity     59
NCBI Description (AC002336) putative potassium transporter [Arabidopsis thaliana]
```

Seq. No.	232174
Seq. ID	LIB3197-048-Q1-M1-C4
Method	BLASTX
NCBI GI	g3868758
BLAST score	460
E value	4.0e-46
Match length	113
% identity	74
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	232175
Seq. ID	LIB3197-048-Q1-M1-D10
Method	BLASTX
NCBI GI	g3236237
BLAST score	403
E value	2.0e-39
Match length	124
% identity	61
NCBI Description	(AC004684) putative ribitol dehydrogenase [Arabidopsis

099016-100

```
Seq. No.      232177
Seq. ID      LIB3197-048-Q1-M1-D6
Method       BLASTX
NCBI GI      g2894612
BLAST score   571
E value      4.0e-59
Match length  128
% identity    77
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      232179
Seq. ID      LIB3197-048-Q1-M1-H2
Method       BLASTX
NCBI GI      g1296805
BLAST score   208
E value      1.0e-16
Match length  55
% identity   64
NCBI Description (X90929) C-terminal peptidase of the D1 protein [Hordeum
vulgare]
```

Seq. No. 232181

Seq. ID LIB3197-048-Q1-M1-H7
 Method BLASTX
 NCBI GI g3282505
 BLAST score 202
 E value 8.0e-16
 Match length 134
 % identity 45
 NCBI Description (AF020786) polyphenol oxidase precursor [Prunus armeniaca]

Seq. No. 232182
 Seq. ID LIB3197-048-Q1-M1-H9
 Method BLASTX
 NCBI GI g2129887
 BLAST score 269
 E value 1.0e-23
 Match length 132
 % identity 45
 NCBI Description major inner envelope protein precursor, 96K, chloroplast - garden pea

Seq. No. 232183
 Seq. ID LIB3197-049-Q1-M1-A1
 Method BLASTX
 NCBI GI g3513738
 BLAST score 327
 E value 2.0e-30
 Match length 91
 % identity 69
 NCBI Description (AF080118). similar to the GDSL family of lipolytic enzymes [Arabidopsis thaliana]

Seq. No. 232184
 Seq. ID LIB3197-049-Q1-M1-A10
 Method BLASTX
 NCBI GI g2618689
 BLAST score 364
 E value 3.0e-35
 Match length 78
 % identity 90
 NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 232185
 Seq. ID LIB3197-049-Q1-M1-A12
 Method BLASTX
 NCBI GI g4239845
 BLAST score 478
 E value 2.0e-48
 Match length 101
 % identity 92
 NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 232186
 Seq. ID LIB3197-049-Q1-M1-A5
 Method BLASTX
 NCBI GI g4455323
 BLAST score 280
 E value 3.0e-25

Match length 72
 % identity 72
 NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 232187
 Seq. ID LIB3197-049-Q1-M1-A7
 Method BLASTX
 NCBI GI g1213629
 BLAST score 342
 E value 4.0e-32
 Match length 93
 % identity 70
 NCBI Description (X95991) pectinesterase [Prunus persica]

Seq. No. 232188
 Seq. ID LIB3197-049-Q1-M1-A9
 Method BLASTX
 NCBI GI g4567235
 BLAST score 365
 E value 8.0e-35
 Match length 114
 % identity 61
 NCBI Description (AC007119) putative phosphatidylinositol/phosphatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No. 232189
 Seq. ID LIB3197-049-Q1-M1-B10
 Method BLASTX
 NCBI GI g3668089
 BLAST score 212
 E value 6.0e-17
 Match length 78
 % identity 47
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 232190
 Seq. ID LIB3197-049-Q1-M1-B2
 Method BLASTX
 NCBI GI g3738320
 BLAST score 257
 E value 4.0e-22
 Match length 123
 % identity 43
 NCBI Description (AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No. 232191
 Seq. ID LIB3197-049-Q1-M1-B3
 Method BLASTX
 NCBI GI g1477468
 BLAST score 114
 E value 7.0e-12
 Match length 85
 % identity 46
 NCBI Description (U35244) vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]

Seq. No.	232197
Seq. ID	LIB3197-049-Q1-M1-C10
Method	BLASTX
NCBI GI	g529516
BLAST score	537
E value	3.0e-55
Match length	99
% identity	89
NCBI Description	(L29099) beta-fructosidase [Solanum tuberosum]
Seq. No.	232198
Seq. ID	LIB3197-049-Q1-M1-C11
Method	BLASTX
NCBI GI	g541951
BLAST score	223
E value	1.0e-18
Match length	70
% identity	66
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]
Seq. No.	232199
Seq. ID	LIB3197-049-Q1-M1-C7
Method	BLASTX
NCBI GI	g4490332
BLAST score	293
E value	2.0e-26
Match length	103
% identity	58
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]
Seq. No.	232200
Seq. ID	LIB3197-049-Q1-M1-C8
Method	BLASTX
NCBI GI	g4101564
BLAST score	223
E value	3.0e-18
Match length	130
% identity	43
NCBI Description	(AF004556) IFA-binding protein [Arabidopsis thaliana]
Seq. No.	232201
Seq. ID	LIB3197-049-Q1-M1-C9
Method	BLASTX
NCBI GI	g2244732
BLAST score	483
E value	9.0e-49
Match length	93
% identity	100
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.	232202
Seq. ID	LIB3197-049-Q1-M1-D12
Method	BLASTX
NCBI GI	g870726
BLAST score	319

E value 1.0e-29
 Match length 84
 % identity 76
 NCBI Description (L38260) biotin carboxylase subunit [Nicotiana tabacum]
 >gi_1582354_prf_2118337A Ac-CoA carboxylase:SUBUNIT=biotin
 carboxylase [Nicotiana tabacum]

Seq. No. 232203
 Seq. ID LIB3197-049-Q1-M1-D2
 Method BLASTX
 NCBI GI g3097321
 BLAST score 196
 E value 3.0e-15
 Match length 88
 % identity 44
 NCBI Description (AB013289) Bd 30K [Glycine max]

Seq. No. 232204
 Seq. ID LIB3197-049-Q1-M1-D4
 Method BLASTX
 NCBI GI g3132696
 BLAST score 436
 E value 2.0e-43
 Match length 98
 % identity 85
 NCBI Description (AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No. 232205
 Seq. ID LIB3197-049-Q1-M1-D6
 Method BLASTX
 NCBI GI g133940
 BLAST score 557
 E value 2.0e-57
 Match length 124
 % identity 92
 NCBI Description 40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir_R3XL3A
 ribosomal protein S3a - African clawed frog
 >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a
 [Xenopus laevis]

Seq. No. 232206
 Seq. ID LIB3197-049-Q1-M1-D9
 Method BLASTX
 NCBI GI g4204300
 BLAST score 188
 E value 3.0e-14
 Match length 72
 % identity 54
 NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 232207
 Seq. ID LIB3197-049-Q1-M1-E1
 Method BLASTX
 NCBI GI g4220512
 BLAST score 188
 E value 4.0e-14
 Match length 57

NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
arietinum]

Seq. No. 232213
Seq. ID LIB3197-049-Q1-M1-F1
Method BLASTX
NCBI GI g3702339
BLAST score 149
E value 9.0e-10
Match length 55
% identity 62
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 232214
Seq. ID LIB3197-049-Q1-M1-F12
Method BLASTX
NCBI GI g2842490
BLAST score 431
E value 1.0e-42
Match length 120
% identity 70
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 232215
Seq. ID LIB3197-049-Q1-M1-F4
Method BLASTX
NCBI GI g4510406
BLAST score 543
E value 9.0e-56
Match length 130
% identity 76
NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No. 232216
Seq. ID LIB3197-049-Q1-M1-F5
Method BLASTX
NCBI GI g2129499
BLAST score 289
E value 6.0e-26
Match length 52
% identity 100
NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton
>gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No. 232217
Seq. ID LIB3197-049-Q1-M1-G5
Method BLASTX
NCBI GI g2558654
BLAST score 365
E value 7.0e-35
Match length 114
% identity 54
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 232218
Seq. ID LIB3197-049-Q1-M1-G6
Method BLASTX

% identity 53
 NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE) >gi_1620013_dbj_BAA12737_ (D85186)
 UDP-glucose:flavonoid-3-glucosyltransferase [Gentiana triflora]

Seq. No. 232229
 Seq. ID LIB3197-050-Q1-M1-B10
 Method BLASTX
 NCBI GI g475048
 BLAST score 609
 E value 2.0e-63
 Match length 132
 % identity 63
 NCBI Description (X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana]

Seq. No. 232230
 Seq. ID LIB3197-050-Q1-M1-B11
 Method BLASTX
 NCBI GI g870726
 BLAST score 379
 E value 2.0e-36
 Match length 93
 % identity 82
 NCBI Description (L38260) biotin carboxylase subunit [Nicotiana tabacum]
 >gi_1582354_prf_2118337A Ac-CoA carboxylase:SUBUNIT=biotin carboxylase [Nicotiana tabacum]

Seq. No. 232231
 Seq. ID LIB3197-050-Q1-M1-B12
 Method BLASTX
 NCBI GI g1351867
 BLAST score 635
 E value 2.0e-66
 Match length 118
 % identity 100
 NCBI Description ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi_761724 (U20114)
 beta-actin [Cricetulus griseus]

Seq. No. 232232
 Seq. ID LIB3197-050-Q1-M1-B3
 Method BLASTX
 NCBI GI g4538939
 BLAST score 697
 E value 8.0e-74
 Match length 140
 % identity 94
 NCBI Description (AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No. 232233
 Seq. ID LIB3197-050-Q1-M1-B6
 Method BLASTX
 NCBI GI g3319921
 BLAST score 277
 E value 1.0e-24

BLAST score 481
 E value 2.0e-48
 Match length 112
 % identity 85
 NCBI Description (AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No. 232283
 Seq. ID LIB3197-051-Q1-M1-D2
 Method BLASTX
 NCBI GI g2244749
 BLAST score 433
 E value 5.0e-43
 Match length 88
 % identity 93
 NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 232284
 Seq. ID LIB3197-051-Q1-M1-D4
 Method BLASTX
 NCBI GI g3687237
 BLAST score 341
 E value 3.0e-32
 Match length 111
 % identity 59
 NCBI Description (AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No. 232285
 Seq. ID LIB3197-051-Q1-M1-D5
 Method BLASTX
 NCBI GI g1362086
 BLAST score 372
 E value 2.0e-38
 Match length 124
 % identity 73
 NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir_S65957
 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No. 232286
 Seq. ID LIB3197-051-Q1-M1-D6
 Method BLASTX
 NCBI GI g3334115
 BLAST score 194
 E value 2.0e-27
 Match length 83
 % identity 78
 NCBI Description ADP,ATP^CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]


```
Seq. No.      232297
Seq. ID      LIB3197-051-Q1-M1-F5-
Method       BLASTX
NCBI GI      g3869088
BLAST score   611
E value      1.0e-63
Match length  117
% identity   100
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
```

```
Seq. No.      232298
Seq. ID      LIB3197-051-Q1-M1-F6
Method       BLASTX
NCBI GI      g2738949
BLAST score   278
E value      3.0e-25
Match length  68
% identity    78
NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x
               ananassa]
```

```
Seq. No.      232299
Seq. ID      LIB3197-051-Q1-M1-F8
Method       BLASTX
NCBI GI      g3024501
BLAST score   494
E value      5.0e-50
Match length  103
% identity    93
NCBI Description  RAS-RELATED PROTEIN RAB11C >gi_1370146_emb_CAA98179_
              (Z73951) RAB11C [Lotus japonicus]
```

```
Seq. No.      232300
Seq. ID      LIB3197-051-Q1-M1-G10
Method       BLASTX
NCBI GI      g1495273
BLAST score   333
E value      4.0e-31
Match length  80
% identity    81
NCBI Description (Z50752) sugar transporter [Arabidopsis thaliana]
```

```
Seq. No.      232301
Seq. ID       LIB3197-051-Q1-M1-G11
Method        BLASTX
NCBI GI       g3341694
BLAST score   516
E value       1.0e-52
Match length  130
% identity    77
NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]
```

```
Seq. No.      232302
Seq. ID      LIB3197-051-Q1-M1-G12
Method       BLASTX
NCBI GI      g4337195
BLAST score   678
```


E value 2.0e-33
 Match length 71
 % identity 93
 NCBI Description (AC005167) putative plasma membrane intrinsic protein
 [Arabidopsis thaliana]

Seq. No. 232318
 Seq. ID LIB3197-052-Q1-M1-A7
 Method BLASTX
 NCBI GI g1155261
 BLAST score 379
 E value 1.0e-36
 Match length 85
 % identity 88
 NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis
 thaliana]

Seq. No. 232319
 Seq. ID LIB3197-052-Q1-M1-A8
 Method BLASTX
 NCBI GI g1703129
 BLAST score 544
 E value 6.0e-56
 Match length 103
 % identity 98
 NCBI Description ACTIN 11 >gi_2129522_pir_S68109 actin 11 - Arabidopsis
 thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis
 thaliana]

Seq. No. 232320
 Seq. ID LIB3197-052-Q1-M1-B1
 Method BLASTX
 NCBI GI g3874433
 BLAST score 220
 E value 7.0e-18
 Match length 106
 % identity 42
 NCBI Description (Z81038) predicted using Genefinder; Similarity to Yeast
 ABD1 protein (SW:P32783); cDNA EST EMBL:T01105 comes from
 this gene [Caenorhabditis elegans]

Seq. No. 232321
 Seq. ID LIB3197-052-Q1-M1-B12
 Method BLASTX
 NCBI GI g2104681
 BLAST score 359
 E value 3.0e-34
 Match length 132
 % identity 60
 NCBI Description (X97907) transcription factor [Vicia faba]

Seq. No. 232322
 Seq. ID LIB3197-052-Q1-M1-B3
 Method BLASTX
 NCBI GI g2832643
 BLAST score 167
 E value 1.0e-11


```
Seq. No.      232328
Seq. ID      LIB3197-052-Q1-M1-C10
Method       BLASTX
NCBI GI      g267069
BLAST score   475
E value      7.0e-48
Match length  93
% identity   95
NCBI Description  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594
                tubulin alpha chain - Arabidopsis thaliana >gi_166914
                (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                (M84697) alpha-4 tubulin [Arabidopsis thaliana]
```

```
Seq. No.      232329
Seq. ID       LIB3197-052-Q1-M1-C2
Method        BLASTX
NCBI GI       g1632831
BLAST score    633
E value       2.0e-66
Match length   135
% identity     93
NCBI Description (Z49698) orf [Ricinus communis]
```

```
Seq. No.      232330
Seq. ID       LIB3197-052-Q1-M1-C4
Method        BLASTX
NCBI GI       g3334113
BLAST score   466
E value       1.0e-46
Match length  89
% identity    100
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015)
                acyl-CoA-binding protein [Gossypium hirsutum]
```

```
Seq. No. 232331
Seq. ID LIB3197-052-Q1-M1-C8
Method BLASTX
NCBI GI g2102696
BLAST score 254
E value 8.0e-22
Match length 146
% identity 40
NCBI Description (U72761) karyopherin beta 3 [Homo sapiens]
>gi_4504909_ref_NP_002262.1_pKPNB3_ karyopherin (importin)
beta
```

```
Seq. No.          232332
Seq. ID           LIB3197-052-Q1-M1-C9
Method            BLASTX
NCBI GI           g730463
BLAST score       322
E value           8.0e-30
Match length      105
% identity        59
NCBI Description   60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
                  >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                  (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
```


[Catharanthus roseus]

Seq. No. 232347
 Seq. ID LIB3197-052-Q1-M1-F11
 Method BLASTX
 NCBI GI g3128175
 BLAST score 142
 E value 7.0e-09
 Match length 88
 % identity 36
 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 232348
 Seq. ID LIB3197-052-Q1-M1-F2
 Method BLASTX
 NCBI GI g2130073
 BLAST score 524
 E value 2.0e-53
 Match length 122
 % identity 85
 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 232349
 Seq. ID LIB3197-052-Q1-M1-F3
 Method BLASTX
 NCBI GI g2130073
 BLAST score 330
 E value 7.0e-31
 Match length 85
 % identity 80
 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 232350
 Seq. ID LIB3197-052-Q1-M1-F5
 Method BLASTX
 NCBI GI g4455192
 BLAST score 380
 E value 1.0e-36
 Match length 140
 % identity 38
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 232351
 Seq. ID LIB3197-052-Q1-M1-F6
 Method BLASTX
 NCBI GI g425194
 BLAST score 573
 E value 3.0e-59
 Match length 121
 % identity 90
 NCBI Description (L26243) heat shock protein [Spinacia oleracea] >gi_2660772

(AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No.	232352
Seq. ID	LIB3197-052-Q1-M1-F7
Method	BLASTX
NCBI GI	g1890281
BLAST score	336
E value	2.0e-31
Match length	103
% identity	22
NCBI Description	(U89984) transformation-sensitive protein homolog [Acanthamoeba castellanii]
Seq. No.	232353
Seq. ID	LIB3197-052-Q1-M1-F8
Method	BLASTX
NCBI GI	g1771780
BLAST score	492
E value	7.0e-50
Match length	125
% identity	82
NCBI Description	(Y10024) ubiquitin extension protein [Solanum tuberosum]
Seq. No.	232354
Seq. ID	LIB3197-052-Q1-M1-F9
Method	BLASTX
NCBI GI	g2827621
BLAST score	411
E value	3.0e-40
Match length	98
% identity	79
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]
Seq. No.	232355
Seq. ID	LIB3197-052-Q1-M1-G10
Method	BLASTX
NCBI GI	g4006893
BLAST score	288
E value	5.0e-26
Match length	60
% identity	92
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
Seq. No.	232356
Seq. ID	LIB3197-052-Q1-M1-G12
Method	BLASTX
NCBI GI	g559713
BLAST score	216
E value	2.0e-17
Match length	108
% identity	40
NCBI Description	(D38552) The ha1539 protein is related to cyclophilin. [Homo sapiens]
Seq. No.	232357
Seq. ID	LIB3197-052-Q1-M1-G4

09631015 101000

```
Seq. No.      232364
Seq. ID      LIB3197-053-Q1-M1-A3
Method       BLASTX
NCBI GI      g1749546
BLAST score   223
E value      4.0e-18
Match length  98
% identity    52
NCBI Description (D89169) similar to Saccharomyces cerevisiae SCD6 protein,
               SWISS-PROT Accession Number P45978 [Schizosaccharomyces
               pombe]
```

```
Seq. No.      232366
Seq. ID      LIB3197-053-Q1-M1-A6
Method       BLASTX
NCBI GI      g2792364
BLAST score   148
E value      2.0e-09
Match length  150
% identity    26
NCBI Description (AF040964) unknown protein IT1 [Homo sapiens]
```

33472

% identity 81
 NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 232368
 Seq. ID LIB3197-053-Q1-M1-A9
 Method BLASTX
 NCBI GI g2494905
 BLAST score 220
 E value 8.0e-18
 Match length 126
 % identity 41
 NCBI Description MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi_2132107_pir_S67174
 hypothetical protein YOR272w - yeast (Saccharomyces
 cerevisiae) >gi_1279699_emb_CAA61778_ (X89633) hypothetical
 protein [Saccharomyces cerevisiae]
 >gi_1420610_emb_CAA99497_ (Z75180) ORF YOR272w
 [Saccharomyces cerevisiae] >gi_1928989 (U92821)
 microtubule-associated protein [Saccharomyces cerevisiae]

Seq. No. 232369
 Seq. ID LIB3197-053-Q1-M1-B2
 Method BLASTX
 NCBI GI g4204695
 BLAST score 276
 E value 1.0e-24
 Match length 118
 % identity 53
 NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase
 At5P1 [Arabidopsis thaliana]

Seq. No. 232370
 Seq. ID LIB3197-053-Q1-M1-B3
 Method BLASTX
 NCBI GI g3355486
 BLAST score 384
 E value 4.0e-37
 Match length 124
 % identity 63
 NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 232371
 Seq. ID LIB3197-053-Q1-M1-B6
 Method BLASTX
 NCBI GI g2983325
 BLAST score 142
 E value 1.0e-08
 Match length 81
 % identity 33
 NCBI Description (AE000705) hypothetical protein [Aquifex aeolicus]

Seq. No. 232372
 Seq. ID LIB3197-053-Q1-M1-C2
 Method BLASTX
 NCBI GI g1705678
 BLAST score 291
 E value 2.0e-26
 Match length 92

% identity 50
 NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
 PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
 valosin-containing protein [Glycine max]

Seq. No. 232373
 Seq. ID LIB3197-053-Q1-M1-C4
 Method BLASTX
 NCBI GI g2244734
 BLAST score 258
 E value 1.0e-22
 Match length 57
 % identity 89
 NCBI Description (D88414) actin [Gossypium hirsutum]

Seq. No. 232374
 Seq. ID LIB3197-053-Q1-M1-C5
 Method BLASTX
 NCBI GI g3914468
 BLAST score 437
 E value 2.0e-43
 Match length 112
 % identity 79
 NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
 >gi_478411_pir_JQ2257 nuclear antigen 21D7 - carrot
 >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus
 carota]

Seq. No. 232375
 Seq. ID LIB3197-053-Q1-M1-C6
 Method BLASTX
 NCBI GI g2789660
 BLAST score 224
 E value 1.0e-18
 Match length 74
 % identity 64
 NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No. 232376
 Seq. ID LIB3197-053-Q1-M1-C7
 Method BLASTX
 NCBI GI g4220535
 BLAST score 152
 E value 6.0e-18
 Match length 121
 % identity 54
 NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis
 thaliana]

Seq. No. 232377
 Seq. ID LIB3197-053-Q1-M1-D11
 Method BLASTX
 NCBI GI g3834321
 BLAST score 439
 E value 1.0e-43
 Match length 134
 % identity 72

Seq. No.	232383
Seq. ID	LIB3197-053-Q1-M1-E7
Method	BLASTX
NCBI GI	g129916
BLAST score	714
E value	9.0e-76
Match length	152
% identity	93
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_(X15232) phosphoglycerate kinase (AA_1 - 401) [Triticum aestivum]
Seq. No.	232384
Seq. ID	LIB3197-053-Q1-M1-F11
Method	BLASTX
NCBI GI	g2281094
BLAST score	463
E value	2.0e-46
Match length	124
% identity	70
NCBI Description	(AC002333) molybdenum cofactor biosynthesis protein E isolog [Arabidopsis thaliana] >gi_4469121_emb_CAB38428_ (AJ133519) molybdopterin synthase large subunit [Arabidopsis thaliana]
Seq. No.	232385
Seq. ID	LIB3197-053-Q1-M1-F12
Method	BLASTX
NCBI GI	g2583108
BLAST score	567
E value	2.0e-58
Match length	152
% identity	76
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.	232386
Seq. ID	LIB3197-053-Q1-M1-F2
Method	BLASTX
NCBI GI	g1332411
BLAST score	270
E value	2.0e-24
Match length	56
% identity	91
NCBI Description	(D85102) dihydroflavonol 4-reductase [Rosa hybrida]
Seq. No.	232387
Seq. ID	LIB3197-053-Q1-M1-F4
Method	BLASTX
NCBI GI	g417060
BLAST score	626
E value	2.0e-65
Match length	121
% identity	94
NCBI Description	GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA LIGASE) (GS) >gi_170637 (M94765) glutamine synthetase

NCBI GI g586076
 BLAST score 668
 E value 2.0e-70
 Match length 125
 % identity 98
 NCBI Description TUBULIN BETA-1 CHAIN >gi_486734_pir_S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No. 232409
 Seq. ID LIB3197-054-Q1-M1-B5
 Method BLASTX
 NCBI GI g1914683
 BLAST score 318
 E value 2.0e-29
 Match length 147
 % identity 51
 NCBI Description (Y12013) RAD23, isoform I [Daucus carota]

Seq. No. 232410
 Seq. ID LIB3197-054-Q1-M1-B6
 Method BLASTX
 NCBI GI g3914467
 BLAST score 142
 E value 1.0e-08
 Match length 90
 % identity 40
 NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum]

Seq. No. 232411
 Seq. ID LIB3197-054-Q1-M1-B7
 Method BLASTX
 NCBI GI g1771780
 BLAST score 526
 E value 9.0e-54
 Match length 132
 % identity 81
 NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 232412
 Seq. ID LIB3197-054-Q1-M1-C10
 Method BLASTX
 NCBI GI g4455192
 BLAST score 225
 E value 2.0e-18
 Match length 125
 % identity 42
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 232413
 Seq. ID LIB3197-054-Q1-M1-C11
 Method BLASTX
 NCBI GI g266463
 BLAST score 750
 E value 5.0e-80

Seq. ID LIB3197-054-Q1-M1-D8
 Method BLASTX
 NCBI GI g1351595
 BLAST score 263
 E value 5.0e-23
 Match length 116
 % identity 43
 NCBI Description HYPOTHETICAL 88.2 KD PROTEIN C4G8.03C IN CHROMOSOME I
 >gi_2130430_pir_S62480 hypothetical protein SPAC4G8.03c -
 fission yeast (Schizosaccharomyces pombe)
 >gi_1022348_emb_CAA91204_ (Z56276) unknown
 [Schizosaccharomyces pombe]

Seq. No. 232424
 Seq. ID LIB3197-054-Q1-M1-E1
 Method BLASTX
 NCBI GI g136739
 BLAST score 329
 E value 1.0e-30
 Match length 99
 % identity 67
 NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
 PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir_XNPOU
 UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
 potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
 pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 232425
 Seq. ID LIB3197-054-Q1-M1-E10
 Method BLASTX
 NCBI GI g267069
 BLAST score 697
 E value 8.0e-74
 Match length 129
 % identity 99
 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594
 tubulin alpha chain - Arabidopsis thaliana >gi_166914
 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 232426
 Seq. ID LIB3197-054-Q1-M1-E11
 Method BLASTX
 NCBI GI g3914467
 BLAST score 316
 E value 2.0e-36
 Match length 127
 % identity 59
 NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
 >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana
 tabacum]

Seq. No. 232427
 Seq. ID LIB3197-054-Q1-M1-E12
 Method BLASTX
 NCBI GI g3912988
 BLAST score 434

FAH1 [Arabidopsis thaliana]

Seq. No. 232468
 Seq. ID LIB3197-055-Q1-M1-F10
 Method BLASTX
 NCBI GI g870726
 BLAST score 450
 E value 7.0e-45
 Match length 109
 % identity 83
 NCBI Description (L38260) biotin carboxylase subunit [Nicotiana tabacum]
 >gi_1582354_prf_2118337A Ac-CoA carboxylase:SUBUNIT=biotin
 carboxylase [Nicotiana tabacum]

Seq. No. 232469
 Seq. ID LIB3197-055-Q1-M1-F12
 Method BLASTX
 NCBI GI g2833389
 BLAST score 617
 E value 2.0e-64
 Match length 138
 % identity 79
 NCBI Description SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III)
 >gi_1200154_emb_CAA65065_ (X95759) glycogen (starch) .
 synthase [Solanum tuberosum]

Seq. No. 232470
 Seq. ID LIB3197-055-Q1-M1-F4
 Method BLASTX
 NCBI GI g4469010
 BLAST score 167
 E value 1.0e-11
 Match length 43
 % identity 72
 NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 232471
 Seq. ID LIB3197-055-Q1-M1-F6
 Method BLASTX
 NCBI GI g729623
 BLAST score 529
 E value 4.0e-54
 Match length 115
 % identity 90
 NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP
 78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG
 5) (BIP 5) >gi_100340_pir_S21880 heat shock protein BiP
 homolog blp5 - common tobacco >gi_19813_emb_CAA42660_
 (X60058) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No. 232472
 Seq. ID LIB3197-055-Q1-M1-G11
 Method BLASTX
 NCBI GI g1916807
 BLAST score 505
 E value 3.0e-51
 Match length 137

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 232478
 Seq. ID LIB3197-055-Q1-M1-H1
 Method BLASTX
 NCBI GI g2583108
 BLAST score 349
 E value 5.0e-33
 Match length 107
 % identity 65
 NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 232479
 Seq. ID LIB3197-055-Q1-M1-H10
 Method BLASTX
 NCBI GI g1174592
 BLAST score 527
 E value 6.0e-54
 Match length 98
 % identity 99
 NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
 - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
 sativum]

Seq. No. 232480
 Seq. ID LIB3197-055-Q1-M1-H2
 Method BLASTX
 NCBI GI g4580394
 BLAST score 332
 E value 5.0e-31
 Match length 95
 % identity 65
 NCBI Description (AC007171) putative fatty acid elongase [Arabidopsis
 thaliana]

Seq. No. 232481
 Seq. ID LIB3197-055-Q1-M1-H3
 Method BLASTX
 NCBI GI g2982259
 BLAST score 566
 E value 2.0e-58
 Match length 129
 % identity 82
 NCBI Description (AF051212) probable 60s ribosomal protein L13a [Picea
 mariana]

Seq. No. 232482
 Seq. ID LIB3197-055-Q1-M1-H4
 Method BLASTX
 NCBI GI g2739383
 BLAST score 486
 E value 4.0e-49
 Match length 114
 % identity 76
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 232483

Seq. ID LIB3197-055-Q1-M1-H6
Method BLASTX
NCBI GI g4469023
BLAST score 415
E value 7.0e-41
Match length 98
% identity 82
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 232484
Seq. ID LIB3197-055-Q1-M1-H7
Method BLASTX
NCBI GI g2494113
BLAST score 436
E value 3.0e-43
Match length 109
% identity 72
NCBI Description (AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No. 232485
Seq. ID LIB3197-055-Q1-M1-H8
Method BLASTX
NCBI GI g2498490
BLAST score 273
E value 4.0e-24
Match length 109
% identity 46
NCBI Description VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556) Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi_4503521_ref_NP_001559.1_pEIF3S6 murine mammary tumor integration site 6 (oncogene homolog)

Seq. No. 232486
Seq. ID LIB3197-055-Q1-M1-H9
Method BLASTX
NCBI GI g2062167
BLAST score 203
E value 5.0e-16
Match length 69
% identity 65
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No. 232487
Seq. ID LIB3197-056-Q1-M1-A10
Method BLASTX
NCBI GI g3548803
BLAST score 573
E value 2.0e-59
Match length 126
% identity 87
NCBI Description (AC005313) putative DNA-binding protein [Arabidopsis

NCBI GI g1170898
 BLAST score 322
 E value 4.0e-30
 Match length 92
 % identity 78
 NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
 >gi_629659_pir_S44167 malate dehydrogenase, mitochondrial
 - cider tree >gi_473206_emb_CAA55383 (X78800)
 mitochondrial malate dehydrogenase [Eucalyptus gunnii]

Seq. No. 232493
 Seq. ID LIB3197-056-Q1-M1-A9
 Method BLASTX
 NCBI GI g2811278
 BLAST score 434
 E value 8.0e-43
 Match length 122
 % identity 74
 NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 232494
 Seq. ID LIB3197-056-Q1-M1-B1
 Method BLASTX
 NCBI GI g2463509
 BLAST score 442
 E value 3.0e-44
 Match length 89
 % identity 89
 NCBI Description (Y09541) pectate lyase [Zinnia elegans]

Seq. No. 232495
 Seq. ID LIB3197-056-Q1-M1-B10
 Method BLASTX
 NCBI GI g2811278
 BLAST score 637
 E value 9.0e-67
 Match length 130
 % identity 88
 NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 232496
 Seq. ID LIB3197-056-Q1-M1-B11
 Method BLASTX
 NCBI GI g1890317
 BLAST score 262
 E value 5.0e-23
 Match length 60
 % identity 78
 NCBI Description (Y11791) peroxidase ATP26a [Arabidopsis thaliana]

Seq. No. 232497
 Seq. ID LIB3197-056-Q1-M1-B12
 Method BLASTX
 NCBI GI g1351303
 BLAST score 245
 E value 6.0e-21
 Match length 62

% identity	61
NCBI Description	(X92491) TOM20 [Solanum tuberosum]
Seq. No.	232503
Seq. ID	LIB3197-056-Q1-M1-C2
Method	BLASTX
NCBI GI	g643469
BLAST score	398
E value	9.0e-39
Match length	138
% identity	57
NCBI Description	(U19886) unknown [Lycopersicon esculentum]
Seq. No.	232504
Seq. ID	LIB3197-056-Q1-M1-C3
Method	BLASTX
NCBI GI	g2213425
BLAST score	512
E value	3.0e-52
Match length	109
% identity	51
NCBI Description	(Z97064) hypothetical protein [Citrus x paradisi]
Seq. No.	232505
Seq. ID	LIB3197-056-Q1-M1-C4
Method	BLASTX
NCBI GI	g2213425
BLAST score	179
E value	3.0e-17
Match length	64
% identity	41
NCBI Description	(Z97064) hypothetical protein [Citrus x paradisi]
Seq. No.	232506
Seq. ID	LIB3197-056-Q1-M1-C5
Method	BLASTX
NCBI GI	g1181333
BLAST score	184
E value	1.0e-13
Match length	40
% identity	78
NCBI Description	(X78057) calreticulin [Zea mays]
Seq. No.	232507
Seq. ID	LIB3197-056-Q1-M1-C8
Method	BLASTX
NCBI GI	g1076746
BLAST score	289
E value	9.0e-37
Match length	99
% identity	76
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]
Seq. No.	232508
Seq. ID	LIB3197-056-Q1-M1-C9


```

NCBI GI          g267079
BLAST score      276
E value          2.0e-24
Match length     52
% identity       100
NCBI Description  TUBULIN BETA-6 CHAIN >gi_320187_pir_JQ1590 tubulin beta-6
                  chain - Arabidopsis thaliana >gi_166904 (M84703) beta-6
                  tubulin [Arabidopsis thaliana]

```

```
Seq. No.      232530
Seq. ID      LIB3197-056-Q1-M1-G1
Method       BLASTX
NCBI GI      g2507281
BLAST score   571
E value      5.0e-59
Match length  104
% identity    100
NCBI Description  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
                (X97380) atran2 [Arabidopsis thaliana]
```

```
Seq. No.      232531
Seq. ID      LIB3197-056-Q1-M1-G3
Method       BLASTX
NCBI GI      g267069
BLAST score   515
E value      2.0e-52
Match length  95
% identity    99
NCBI Description  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
```

```
Seq. No.      232532
Seq. ID      LIB3197-056-Q1-M1-G7
Method       BLASTX
NCBI GI      g3914996
BLAST score   160
E value      4.0e-11
Match length  78
% identity    51
NCBI Description  PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
                  >gi_1665831_dbj_BAA13640_ (D88541) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi_2804260_dbj_BAA24441_ (AB010408) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi_3367581_emb_CAA20033_ (AL031135) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
```

```
Seq. No.          232533
Seq. ID           LIB3197-056-Q1-M1-G8
Method            BLASTX
NCBI GI           g267069
BLAST score       437
E value           2.0e-43
Match length      86
% identity        94
```



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NCBI GI      g4097579
BLAST score  565
E value      2.0e-58
Match length 117
% identity   86
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

```

```
Seq. No.      232544
Seq. ID      LIB3197-057-Q1-M1-A7
Method       BLASTX
NCBI GI      g232029
BLAST score   144
E value      7.0e-13
Match length  119
% identity   42
NCBI Description  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                >gi_100154_pir_S21989 translation elongation factor eEF-1
                alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)
                elongation factor 1A [Daucus carota]
```

```
Seq. No.      232545
Seq. ID      LIB3197-057-Q1-M1-A8
Method       BLASTX
NCBI GI      g2104529
BLAST score   529
E value      4.0e-54
Match length  135
% identity    78
NCBI Description (AF001308) putative hexose transporter [Arabidopsis
thaliana]
```

```
Seq. No.          232546
Seq. ID           LIB3197-057-Q1-M1-A9
Method            BLASTX
NCBI GI           gi1076660
BLAST score       380
E value           1.0e-36
Match length      104
% identity         74
NCBI Description   D13F(MYBST1) protein - potato >gi_786426_bbs_159122
                  {S74753} MybSt1=Myb-related transcriptional activator
                  {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                  leaf, Peptide, 342 aa] [Solanum tuberosum]
```

Seq. No.	232547
Seq. ID	LIB3197-057-Q1-M1-B1
Method	BLASTX
NCBI GI	g1839188
BLAST score	540
E value	2.0e-55
Match length	140
% identity	74
NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]

```
Seq. No.      232548
Seq. ID      LIB3197-057-Q1-M1-B11
Method      BLASTX
```


E value 3.0e-28
 Match length 79
 % identity 38
 NCBI Description (AF118222) contains similarity to RNA recognition motifs
 (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
 >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
 [Arabidopsis thaliana]

Seq. No. 232554
 Seq. ID LIB3197-057-Q1-M1-C11
 Method BLASTX
 NCBI GI g2342724
 BLAST score 554
 E value 4.0e-57
 Match length 135
 % identity 79
 NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 232555
 Seq. ID LIB3197-057-Q1-M1-C12
 Method BLASTX
 NCBI GI g549063
 BLAST score 387
 E value 1.0e-37
 Match length 113
 % identity 67
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1072464_pir_A38958 IgE-dependent histamine-releasing
 factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
 21kd polypeptide [Oryza sativa]

Seq. No. 232556
 Seq. ID LIB3197-057-Q1-M1-C3
 Method BLASTX
 NCBI GI g3892051
 BLAST score 133
 E value 1.0e-17
 Match length 57
 % identity 81
 NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit
 [Arabidopsis thaliana]

Seq. No. 232557
 Seq. ID LIB3197-057-Q1-M1-C6
 Method BLASTX
 NCBI GI g3757514
 BLAST score 386
 E value 2.0e-37
 Match length 90
 % identity 82
 NCBI Description (AC005167) putative plasma membrane intrinsic protein
 [Arabidopsis thaliana]

Seq. No. 232558
 Seq. ID LIB3197-057-Q1-M1-C8
 Method BLASTX
 NCBI GI g4455221

BLAST score 350
 E value 4.0e-33
 Match length 89
 % identity 78
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 232559
 Seq. ID LIB3197-057-Q1-M1-D11
 Method BLASTX
 NCBI GI g3047085
 BLAST score 447
 E value 2.0e-44
 Match length 132
 % identity 66
 NCBI Description (AF058914) No definition line found [Arabidopsis thaliana]

Seq. No. 232560
 Seq. ID LIB3197-057-Q1-M1-D12
 Method BLASTX
 NCBI GI g4490330
 BLAST score 744
 E value 3.0e-79
 Match length 144
 % identity 94
 NCBI Description (AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No. 232561
 Seq. ID LIB3197-057-Q1-M1-D2
 Method BLASTX
 NCBI GI g4580394
 BLAST score 267
 E value 2.0e-23
 Match length 123
 % identity 42
 NCBI Description (AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No. 232562
 Seq. ID LIB3197-057-Q1-M1-D4
 Method BLASTX
 NCBI GI g2462827
 BLAST score 220
 E value 5.0e-18
 Match length 64
 % identity 70
 NCBI Description (AF000657) probable thiamin biosynthetic enzyme [Arabidopsis thaliana]

Seq. No. 232563
 Seq. ID LIB3197-057-Q1-M1-D8
 Method BLASTX
 NCBI GI g2062167
 BLAST score 442
 E value 7.0e-44
 Match length 102
 % identity 80

NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
(CCT-ALPHA) >gi_322602_pir_JN0448 t-complex polypeptide
Tcpl - Arabidopsis thaliana >gi_217871_dbj_BAA01955_
(D11351) t-complex polypeptide 1 homologue [Arabidopsis
thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 232590
Seq. ID LIB3197-057-Q1-M1-H6
Method BLASTX
NCBI GI g1931647
BLAST score 320
E value 1.0e-29
Match length 86
% identity 71
NCBI Description (U95973) endomembrane protein EMP70 precursor isolog
[Arabidopsis thaliana]

Seq. No. 232591
Seq. ID LIB3197-057-Q1-M1-H8
Method BLASTX
NCBI GI g3687237
BLAST score 227
E value 7.0e-19
Match length 100
% identity 53
NCBI Description (AC005169) putative Cys3His zinc-finger protein
[Arabidopsis thaliana]

Seq. No. 232592
Seq. ID LIB3197-058-Q1-M1-B1
Method BLASTX
NCBI GI g1663706
BLAST score 192
E value 1.0e-14
Match length 92
% identity 47
NCBI Description (D87685) similar to human transcription factor TFIIS
(S34159). [Homo sapiens]

Seq. No. 232593
Seq. ID LIB3197-058-Q1-M1-B2
Method BLASTX
NCBI GI g4220476
BLAST score 200
E value 2.0e-16
Match length 87
% identity 60
NCBI Description (AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No. 232594
Seq. ID LIB3197-058-Q1-M1-C3
Method BLASTX
NCBI GI g3025299
BLAST score 149
E value 2.0e-09
Match length 116

% identity	31
NCBI Description	HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi_2088660 (AF002109) ABC1 isolog [Arabidopsis thaliana]
Seq. No.	232595
Seq. ID	LIB3197-058-Q1-M1-C7
Method	BLASTX
NCBI GI	g113116
BLAST score	391
E value	6.0e-38
Match length	140
% identity	52
NCBI Description	ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) >gi_111396_pir_A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase [Rattus norvegicus]
Seq. No.	232596
Seq. ID	LIB3197-058-Q1-M1-D1
Method	BLASTX
NCBI GI	g3193284
BLAST score	235
E value	9.0e-20
Match length	116
% identity	37
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]
Seq. No.	232597
Seq. ID	LIB3197-058-Q1-M1-D2
Method	BLASTX
NCBI GI	g4559310
BLAST score	151
E value	8.0e-10
Match length	133
% identity	29
NCBI Description	(AF129131) putative Zic3 binding protein; CBP3 protein homolog [Xenopus laevis]
Seq. No.	232598
Seq. ID	LIB3197-058-Q1-M1-D3
Method	BLASTX
NCBI GI	g3702962
BLAST score	309
E value	3.0e-28
Match length	61
% identity	95
NCBI Description	(AF079484) rac GTP binding protein Arac7 [Arabidopsis thaliana]
Seq. No.	232599
Seq. ID	LIB3197-058-Q1-M1-D9
Method	BLASTX
NCBI GI	g2444178
BLAST score	689
E value	7.0e-73
Match length	140
% identity	91

NCBI Description (U94784) unconventional myosin [Helianthus annuus]

Seq. No. 232600
Seq. ID LIB3197-058-Q1-M1-E9
Method BLASTX
NCBI GI g125887
BLAST score 110
E value 1.0e-09
Match length 86
% identity 49
NCBI Description ANOTHER SPECIFIC LAT52 PROTEIN PRECURSOR
>gi_82092_pir_S04765 LAT52 protein precursor - tomato
>gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
esculentum]

Seq. No. 232601
Seq. ID LIB3197-058-Q1-M1-F1
Method BLASTX
NCBI GI g1174592
BLAST score 548
E value 2.0e-56
Match length 120
% identity 86
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
- garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
sativum]

Seq. No. 232602
Seq. ID LIB3197-058-Q1-M1-F7
Method BLASTX
NCBI GI g4337175
BLAST score 433
E value 7.0e-43
Match length 123
% identity 67
NCBI Description (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 232603
Seq. ID LIB3197-058-Q1-M1-F8
Method BLASTX
NCBI GI g972511
BLAST score 141
E value 1.0e-18
Match length 60
% identity 87
NCBI Description (X90982) phosphoenolpyruvate carboxylase [Solanum
tuberosum]

Seq. No. 232604
Seq. ID LIB3197-058-Q1-M1-G1
Method BLASTX
NCBI GI g1354849
BLAST score 293
E value 9.0e-33

Seq. No.	232620
Seq. ID	LIB3197-059-Q1-M1-B1
Method	BLASTX
NCBI GI	g3643598
BLAST score	657
E value	4.0e-69
Match length	146
% identity	84
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]
Seq. No.	232621
Seq. ID	LIB3197-059-Q1-M1-B4
Method	BLASTX
NCBI GI	g4567250
BLAST score	196
E value	5.0e-15
Match length	86
% identity	55
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.	232622
Seq. ID	LIB3197-059-Q1-M1-B7
Method	BLASTX
NCBI GI	g3319355
BLAST score	535
E value	7.0e-55
Match length	125
% identity	91
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]
Seq. No.	232623
Seq. ID	LIB3197-059-Q1-M1-B8
Method	BLASTX
NCBI GI	g4432845
BLAST score	158
E value	1.0e-10
Match length	85
% identity	45
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.	232624
Seq. ID	LIB3197-059-Q1-M1-B9
Method	BLASTX
NCBI GI	g584867
BLAST score	166
E value	1.0e-11
Match length	113
% identity	33
NCBI Description	CYTOCHROME P450 77A2 (CYPLXXVIIA2) (P-450EG5) >gi_481959_pir_S40266 gene CYP77A2 protein - eggplant >gi_542071_pir_S41598 cytochrome P450 77A2 - eggplant >gi_438241_emb_CAA50646_ (X71655) CYP77A2 [Solanum melongena]

(AJ222771) T protein [Pisum sativum]

Seq. No. 232640
 Seq. ID LIB3197-059-Q1-M1-G1
 Method BLASTX
 NCBI GI g2288981
 BLAST score 300
 E value 3.0e-27
 Match length 89
 % identity 39
 NCBI Description (AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi 3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No. 232641
 Seq. ID LIB3197-059-Q1-M1-G11
 Method BLASTX
 NCBI GI g3702332
 BLAST score 251
 E value 1.0e-21
 Match length 81
 % identity 58
 NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 232642
 Seq. ID LIB3197-059-Q1-M1-G12
 Method BLASTX
 NCBI GI g3738297
 BLAST score 271
 E value 7.0e-24
 Match length 92
 % identity 28
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 232643
 Seq. ID LIB3197-059-Q1-M1-G3
 Method BLASTX
 NCBI GI g1477428
 BLAST score 615
 E value 3.0e-64
 Match length 140
 % identity 85
 NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 232644
 Seq. ID LIB3197-059-Q1-M1-G5
 Method BLASTX
 NCBI GI g3063710
 BLAST score 498
 E value 2.0e-50
 Match length 144
 % identity 66
 NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 232645
 Seq. ID LIB3197-059-Q1-M1-G6
 Method BLASTX

NCBI Description tubulin beta-1 chain - rice

Seq. No. 232656
Seq. ID LIB3197-059-Q1-M1-H9
Method BLASTX
NCBI GI g3169287
BLAST score 166
E value 1.0e-11
Match length 52
% identity 65

NCBI Description (AF050673) vacuolar H⁺-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No. 232657
Seq. ID LIB3197-060-Q1-M1-A10
Method BLASTX
NCBI GI g1172872
BLAST score 310
E value 2.0e-28
Match length 132
% identity 56

NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir_JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 232658
Seq. ID LIB3197-060-Q1-M1-A11
Method BLASTX
NCBI GI g1076746
BLAST score 652
E value 3.0e-69
Match length 147
% identity 97

NCBI Description heat shock protein 70 - rice (fragment)
>gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No. 232659
Seq. ID LIB3197-060-Q1-M1-A2
Method BLASTX
NCBI GI g586076
BLAST score 528
E value 5.0e-54
Match length 105
% identity 88

NCBI Description TUBULIN BETA-1 CHAIN >gi_486734_pir_S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No. 232660
Seq. ID LIB3197-060-Q1-M1-A3
Method BLASTX
NCBI GI g1172872
BLAST score 264

BLAST score 241
 E value 2.0e-20
 Match length 55
 % identity 67
 NCBI Description (AC005396) gibberellin-regulated protein GAST1-like
 [Arabidopsis thaliana]

Seq. No. 232666
 Seq. ID LIB3197-060-Q1-M1-B5
 Method BLASTX
 NCBI GI g2384671
 BLAST score 578
 E value 8.0e-60
 Match length 150
 % identity 74
 NCBI Description (AF012657) putative potassium transporter AtKT2p
 [Arabidopsis thaliana]

Seq. No. 232667
 Seq. ID LIB3197-060-Q1-M1-B7
 Method BLASTX
 NCBI GI g1245343
 BLAST score 226
 E value 1.0e-18
 Match length 65
 % identity 62
 NCBI Description (U50194) tripeptidylpeptidase II [Rattus norvegicus]

Seq. No. 232668
 Seq. ID LIB3197-060-Q1-M1-B8
 Method BLASTX
 NCBI GI g1777921
 BLAST score 615
 E value 3.0e-64
 Match length 126
 % identity 93
 NCBI Description (U54774) glutamate decarboxylase [Nicotiana tabacum]

Seq. No. 232669
 Seq. ID LIB3197-060-Q1-M1-C10
 Method BLASTX
 NCBI GI g2832625
 BLAST score 431
 E value 1.0e-42
 Match length 102
 % identity 81
 NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 232670
 Seq. ID LIB3197-060-Q1-M1-C11
 Method BLASTX
 NCBI GI g3023271
 BLAST score 691
 E value 4.0e-73
 Match length 140
 % identity 95
 NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)


```
Seq. ID          LIB3197-060-Q1-M1-E3
Method           BLASTX
NCBI GI          g2497492
BLAST score      240
E value          9.0e-26
Match length     121
% identity       55
NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
                  KINASE) >gi_1653646_dbj_BAA18558_(D90915) uridine
                  monophosphate kinase [Synechocystis sp.]
```

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Seq. No.      232692
Seq. ID       LIB3197-060-Q1-M1-E6
Method        BLASTX
NCBI GI       g2129578
BLAST score    227
E value       8.0e-19
Match length   63
% identity     75
NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of
dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
>gi_1585435_prf_2124427B diamide resistance gene
[Arabidopsis thaliana]
```

```
Seq. No.      232693
Seq. ID      LIB3197-060-Q1-M1-E7
Method       BLASTX
NCBI GI      g2880051
BLAST score   167
E value      1.0e-11
Match length  64
% identity    53
NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]
```

```
Seq. No.      232694
Seq. ID       LIB3197-060-Q1-M1-E8
Method        BLASTX
NCBI GI       g134891
BLAST score   142
E value       9.0e-09
Match length  99
% identity    35
NCBI Description  SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
                (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                >gi_89066_pir_A24570 signal recognition particle receptor
                precursor - dog >gi_997_emb_CAA26945_ (X03184) signal
                recognition particle receptor [Canis sp.]
                >gi_224778_prf_1112224A signal recognition particle
                receptor [Canis familiaris]
```

Seq. No.	232695
Seq. ID	LIB3197-060-Q1-M1-F12
Method	BLASTX
NCBI GI	g484656
BLAST score	599
E value	3.0e-62

Seq. No. 232711
 Seq. ID LIB3197-060-Q1-M1-H7
 Method BLASTX
 NCBI GI g1174592
 BLAST score 540
 E value 2.0e-55
 Match length 103
 % identity 99
 NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
 - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
 sativum]

Seq. No. 232712
 Seq. ID LIB3197-060-Q1-M1-H8
 Method BLASTX
 NCBI GI g1172556
 BLAST score 390
 E value 8.0e-38
 Match length 91
 % identity 79
 NCBI Description 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
 (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
 (POM 36) >gi_629729_pir_S46925 porin II, 36K - potato
 >gi_1076681_pir_B55364 porin (clone pPOM 36.2) - potato
 mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin
 II [Solanum tuberosum]

Seq. No. 232713
 Seq. ID LIB3272-001-P1-K1-A10
 Method BLASTX
 NCBI GI g421923
 BLAST score 386
 E value 2.0e-37
 Match length 94
 % identity 70
 NCBI Description pathogenesis-related protein P23 - tomato (fragment)
 >gi_542031_pir_PQ0742 pathogenesis-related protein P23
 precursor - tomato (fragment) >gi_19315_emb_CAA50059_
 (X70787) pathogenesis-related protein PR P23 [Lycopersicon
 esculentum]

Seq. No. 232714
 Seq. ID LIB3272-001-P1-K1-A11
 Method BLASTX
 NCBI GI g4218122
 BLAST score 332
 E value 5.0e-31
 Match length 120
 % identity 57
 NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 232715
 Seq. ID LIB3272-001-P1-K1-A4
 Method BLASTX
 NCBI GI g3287824
 BLAST score 524

0988016-101000

```
Seq. No.      232738
Seq. ID       LIB3272-001-P1-K1-D6
Method        BLASTX
NCBI GI       g4567307
BLAST score   207
E value       2.0e-16
Match length  102
% identity    45
NCBI Description (AC005956) putative zinc finger protein [Arabidopsis thaliana]
```

```
Seq. No.      232739
Seq. ID      LIB3272-001-P1-K1-D7
Method       BLASTX
NCBI GI      g131772
BLAST score   288
E value      7.0e-26
Match length  74
% identity    81
NCBI Description  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
                >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                maize
```

```
Seq. No.          232740
Seq. ID           LIB3272-001-P1-K1-D9
Method            BLASTX
NCBI GI           g3915873
BLAST score       714
E value           8.0e-76
Match length      136
% identity        96
NCBI Description  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
                  (NODULIN-100) >gi_2606081 (AF030231) sucrose synthase
                  [Glycine max]
```

```
Seq. No.      232741
Seq. ID       LIB3272-001-P1-K1-E1
Method        BLASTX
NCBI GI       g3063396
BLAST score    525
E value       1.0e-53
Match length   118
% identity     84
NCBI Description (AB012947) vcCyP [Vicia faba]
```


Seq. ID LIB3272-001-P1-K1-E6
 Method BLASTX
 NCBI GI g4510346
 BLAST score 168
 E value 8.0e-12
 Match length 38
 % identity 87
 NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 232748
 Seq. ID LIB3272-001-P1-K1-E7
 Method BLASTX
 NCBI GI g3868758
 BLAST score 445
 E value 3.0e-44
 Match length 108
 % identity 75
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 232749
 Seq. ID LIB3272-001-P1-K1-E9
 Method BLASTX
 NCBI GI g1174592
 BLAST score 713
 E value 1.0e-75
 Match length 135
 % identity 98
 NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
 - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
 sativum]

Seq. No. 232750
 Seq. ID LIB3272-001-P1-K1-F1
 Method BLASTX
 NCBI GI g4337046
 BLAST score 308
 E value 3.0e-28
 Match length 118
 % identity 57
 NCBI Description (AF124162) molybdopterin synthase sulphurylase [Nicotiana
 plumbaginifolia]

Seq. No. 232751
 Seq. ID LIB3272-001-P1-K1-F11
 Method BLASTX
 NCBI GI g3420239
 BLAST score 333
 E value 3.0e-31
 Match length 63
 % identity 100
 NCBI Description (AF059484) actin [Gossypium hirsutum]

Seq. No. 232752
 Seq. ID LIB3272-001-P1-K1-F12
 Method BLASTX
 NCBI GI g4455323
 BLAST score 356

09684016-101000

Seq. No. 232763
 Seq. ID LIB3272-001-P1-K1-G6
 Method BLASTX
 NCBI GI g267082
 BLAST score 632
 E value 3.0e-66
 Match length 118
 % identity 98
 NCBI Description TUBULIN BETA-8 CHAIN >gi_320189_pir_JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No. 232764
 Seq. ID LIB3272-001-P1-K1-G7
 Method BLASTX
 NCBI GI g3878594
 BLAST score 109
 E value 3.0e-10
 Match length 106
 % identity 34
 NCBI Description (Z81102) Similarity to Mouse CMP-sialic acid transporter (TR:Q61420) [Caenorhabditis elegans]
 >gi_3881872_emb_CAB05329_ (Z82288) Similarity to Mouse CMP-sialic acid transporter (TR:Q61420) [Caenorhabditis elegans]

Seq. No. 232765
 Seq. ID LIB3272-001-P1-K1-G8
 Method BLASTX
 NCBI GI g2493131
 BLAST score 503
 E value 4.0e-51
 Match length 106
 % identity 95
 NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No. 232766
 Seq. ID LIB3272-001-P1-K1-G9
 Method BLASTX
 NCBI GI g3901014
 BLAST score 235
 E value 1.0e-19
 Match length 55
 % identity 76
 NCBI Description (AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No. 232767
 Seq. ID LIB3272-001-P1-K1-H10
 Method BLASTX
 NCBI GI g4521249
 BLAST score 442
 E value 6.0e-44
 Match length 111

% identity 73
 NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 232784
 Seq. ID LIB3272-002-P1-K1-B5
 Method BLASTX
 NCBI GI g4056502
 BLAST score 432
 E value 9.0e-43
 Match length 103
 % identity 83
 NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No. 232785
 Seq. ID LIB3272-002-P1-K1-B7
 Method BLASTX
 NCBI GI g1173256
 BLAST score 633
 E value 3.0e-66
 Match length 123
 % identity 98
 NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No. 232786
 Seq. ID LIB3272-002-P1-K1-C10
 Method BLASTX
 NCBI GI g2160166
 BLAST score 466
 E value 9.0e-47
 Match length 135
 % identity 62
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 232787
 Seq. ID LIB3272-002-P1-K1-C12
 Method BLASTX
 NCBI GI g2351380
 BLAST score 235
 E value 1.0e-19
 Match length 96
 % identity 54
 NCBI Description (U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens] >gi_4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN

Seq. No. 232788
 Seq. ID LIB3272-002-P1-K1-C5
 Method BLASTX
 NCBI GI g1326338
 BLAST score 178
 E value 4.0e-13
 Match length 85
 % identity 46
 NCBI Description (U58746) R05G6.4 gene product [Caenorhabditis elegans]

0968075-1000

```
Seq. No.      232801
Seq. ID      LIB3272-002-P1-K1-E3
Method       BLASTX
NCBI GI      g2435604
BLAST score   117
E value      5.0e-09
Match length  65
% identity    48
NCBI Description (AF026213) strong similarity to Saccharomyces cerevisiae
               endosomal P24A protein (SP:P32802) [Caenorhabditis elegans]
```

```
Seq. No.      232803
Seq. ID      LIB3272-002-P1-K1-E5
Method       BLASTX
NCBI GI      g480450
BLAST score   418
E value      4.0e-41
Match length  114
% identity    75
NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid
reductoisomerase [Arabidopsis thaliana]
```

33558

E value	2.0e-45
Match length	136
% identity	65
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_2129912_pir_S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi_1184668 (U22147) beta-1,3-glucanase [Hevea brasiliensis]
Seq. No.	232810
Seq. ID	LIB3272-002-P1-K1-F2
Method	BLASTX
NCBI GI	g3913633
BLAST score	363
E value	1.0e-34
Match length	113
% identity	66
NCBI Description	HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown protein [Arabidopsis thaliana]
Seq. No.	232811
Seq. ID	LIB3272-002-P1-K1-F3
Method	BLASTX
NCBI GI	g2501647
BLAST score	476
E value	6.0e-48
Match length	127
% identity	75
NCBI Description	UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi_1362120_pir_S55732 uroporphyrinogen decarboxylase - common tobacco >gi_1009429_emb_CAA58040_ (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]
Seq. No.	232812
Seq. ID	LIB3272-002-P1-K1-F4
Method	BLASTX
NCBI GI	g2244806
BLAST score	257
E value	3.0e-22
Match length	92
% identity	55
NCBI Description	(297336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	232813
Seq. ID	LIB3272-002-P1-K1-F5
Method	BLASTX
NCBI GI	g549063
BLAST score	506
E value	2.0e-51
Match length	117
% identity	82
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	232814
Seq. ID	LIB3272-002-P1-K1-F7
Method	BLASTX
NCBI GI	g3158376
BLAST score	473
E value	1.0e-47
Match length	125
% identity	76
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]
Seq. No.	232815
Seq. ID	LIB3272-002-P1-K1-F8
Method	BLASTX
NCBI GI	g1917019
BLAST score	549
E value	2.0e-56
Match length	114
% identity	90
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]
Seq. No.	232816
Seq. ID	LIB3272-002-P1-K1-F9
Method	BLASTX
NCBI GI	g2911362
BLAST score	245
E value	1.0e-22
Match length	118
% identity	58
NCBI Description	(AF041045) NADPH HC toxin reductase [Zea mays]
Seq. No.	232817
Seq. ID	LIB3272-002-P1-K1-G1
Method	BLASTX
NCBI GI	g3694872
BLAST score	461
E value	4.0e-46
Match length	112
% identity	78
NCBI Description	(AF092547) profilin [Ricinus communis]
Seq. No.	232818
Seq. ID	LIB3272-002-P1-K1-G10
Method	BLASTX
NCBI GI	g3668089
BLAST score	217
E value	1.0e-17
Match length	80
% identity	47
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	232819
Seq. ID	LIB3272-002-P1-K1-G11
Method	BLASTX
NCBI GI	g2662343
BLAST score	601
E value	1.0e-62
Match length	117

% identity 98
 NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 232820
 Seq. ID LIB3272-002-P1-K1-G12
 Method BLASTX
 NCBI GI g729470
 BLAST score 497
 E value 2.0e-50
 Match length 122
 % identity 80
 NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
 (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
 >gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2)
 precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
 (Z21493) mitochondrial formate dehydrogenase precursor
 [Solanum tuberosum]

Seq. No. 232821
 Seq. ID LIB3272-002-P1-K1-G2
 Method BLASTX
 NCBI GI g218157
 BLAST score 594
 E value 9.0e-62
 Match length 134
 % identity 88
 NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No. 232822
 Seq. ID LIB3272-002-P1-K1-G5
 Method BLASTX
 NCBI GI g886100
 BLAST score 454
 E value 2.0e-45
 Match length 97
 % identity 88
 NCBI Description (U27347) putative water channel protein; plasmalemma
 intrinsic protein; similar to Arabidopsis Pip2a gene
 product, PIR Accession Number S44084 [Glycine max]

Seq. No. 232823
 Seq. ID LIB3272-002-P1-K1-G7
 Method BLASTX
 NCBI GI g3420004
 BLAST score 243
 E value 1.0e-20
 Match length 118
 % identity 43
 NCBI Description (AF000305) steroid sulfotransferase 1 [Brassica napus]

Seq. No. 232824
 Seq. ID LIB3272-002-P1-K1-G9
 Method BLASTX
 NCBI GI g1076510
 BLAST score 635
 E value 1.0e-66
 Match length 136

% identity 85
 NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
 >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus
 vulgaris]

Seq. No. 232825
 Seq. ID LIB3272-002-P1-K1-H10
 Method BLASTX
 NCBI GI g3668089
 BLAST score 182
 E value 2.0e-13
 Match length 86
 % identity 42
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 232826
 Seq. ID LIB3272-002-P1-K1-H11
 Method BLASTX
 NCBI GI g120669
 BLAST score 484
 E value 6.0e-49
 Match length 120
 % identity 78
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
 dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
 >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 232827
 Seq. ID LIB3272-002-P1-K1-H12
 Method BLASTX
 NCBI GI g4454097
 BLAST score 273
 E value 4.0e-24
 Match length 66
 % identity 82
 NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]

Seq. No. 232828
 Seq. ID LIB3272-002-P1-K1-H2
 Method BLASTX
 NCBI GI g1169782
 BLAST score 255
 E value 5.0e-22
 Match length 101
 % identity 57
 NCBI Description FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis
 thaliana]

Seq. No. 232829
 Seq. ID LIB3272-002-P1-K1-H3
 Method BLASTX
 NCBI GI g1170747
 BLAST score 296
 E value 8.0e-27
 Match length 72

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0964-0738-2000-00000000

0964-0738-2000-00000000

0968-0767(199609)16:03;1-P

```
Seq. No.      232841
Seq. ID      LIB3272-003-P1-K1-B12
Method       BLASTX
NCBI GI      g3176684
BLAST score   380
E value      1.0e-36
Match length  131
% identity    57
NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside
transporter 1 gb_U81375 from Homo sapiens. ESTs gb_N65317,
gb_T20785, gb_AA586285 and gb_AA712578 come from this gene.
[Arabidopsis thaliana]
```

```
Seq. No.      232843
Seq. ID       LIB3272-003-P1-K1-B4
Method        BLASTX
NCBI GI       g3927825
BLAST score   513
E value       3.0e-52
Match length  100
% identity    95
NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase
```


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```
Seq. No.      232845
Seq. ID      LIB3272-003-P1-K1-B7
Method       BLASTX
NCBI GI      g2914698
BLAST score   196
E value      4.0e-15
Match length  101
% identity    46
NCBI Description (AC003974) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.          232846
Seq. ID           LIB3272-003-P1-K1-B8
Method            BLASTX
NCBI GI           g1166450
BLAST score       299
E value           4.0e-27
Match length      67
% identity        79
NCBI Description   (X95262) Tfm5 [Lycopersicon esculentum]
```

```
Seq. No.      232847
Seq. ID      LIB3272-003-P1-K1-C2
Method       BLASTX
NCBI GI      g3860247
BLAST score   550
E value      1.0e-56
Match length  114
% identity    88
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
```

Seq. No.	232848
Seq. ID	LIB3272-003-P1-K1-C3
Method	BLASTX
NCBI GI	g4220481
BLAST score	154
E value	3.0e-10
Match length	43
% identity	65
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

```
Seq. No.      232849
Seq. ID       LIB3272-003-P1-K1-C4
Method        BLASTX
NCBI GI       g1703108
BLAST score   508
```


E value 1.0e-51
 Match length 93
 % identity 100
 NCBI Description ACTIN 2/7 >gi_2129525_pir_S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir_S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No. 232850
 Seq. ID LIB3272-003-P1-K1-C5
 Method BLASTX
 NCBI GI g4263517
 BLAST score 407
 E value 8.0e-40
 Match length 128
 % identity 64
 NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana]

Seq. No. 232851
 Seq. ID LIB3272-003-P1-K1-C6
 Method BLASTX
 NCBI GI g729668
 BLAST score 329
 E value 1.0e-30
 Match length 76
 % identity 86
 NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No. 232852
 Seq. ID LIB3272-003-P1-K1-C9
 Method BLASTX
 NCBI GI g1129145
 BLAST score 591
 E value 2.0e-61
 Match length 129
 % identity 87
 NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No. 232853
 Seq. ID LIB3272-003-P1-K1-D1
 Method BLASTX
 NCBI GI g1928981
 BLAST score 549
 E value 2.0e-56
 Match length 114
 % identity 95
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 232854
 Seq. ID LIB3272-003-P1-K1-D10


```

NCBI GI      g585241
BLAST score   237
E value       7.0e-20
Match length  61
% identity    77
NCBI Description HISTONE H1 >gi_629668_pir_S45662 histone H1 - tomato
                >gi_424100 (U03391) histone H1 [Lycopersicon esculentum]

```

```
Seq. No.      232860
Seq. ID      LIB3272-003-P1-K1-E12
Method       BLASTX
NCBI GI      g1173256
BLAST score   626
E value      2.0e-65
Match length  123
% identity    98
NCBI Description  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal
protein S4 - upland cotton >gi_488739_emb_CAA55882_
(X79300) ribosomal protein, small subunit 4e (RS4e)
[Gossypium hirsutum]
```

```
Seq. No.      232861
Seq. ID      LIB3272-003-P1-K1-E2
Method       BLASTX
NCBI GI      g2160166
BLAST score   332
E value      5.0e-31
Match length  131
% identity    57
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
```

```
Seq. No.      232862
Seq. ID      LIB3272-003-P1-K1-E3
Method       BLASTX
NCBI GI      g3006145
BLAST score   379
E value      1.0e-36
Match length  131
% identity    35
NCBI Description (AL022299) ABC transporter [Schizosaccharomyces pombe]
```

```
Seq. No.          232863
Seq. ID          LIB3272-003-P1-K1-E7
Method           BLASTX
NCBI GI         g3861068
BLAST score      176
E value         1.0e-12
Match length     60
% identity       50
NCBI Description (AJ235272) unknown [Rickettsia prowazekii]
```

```
Seq. No.      232864
Seq. ID      LIB3272-003-P1-K1-E9
Method      BLASTX
NCBI GI      g456568
BLAST score   737
E value      2.0e-78
```



```
BLAST score      500
E value         1.0e-50
Match length    119
% identity      79
NCBI Description (AF092547) profilin [Ricinus communis]
```

```
Seq. No.      232870
Seq. ID      LIB3272-003-P1-K1-F3
Method       BLASTX
NCBI GI      g1709498
BLAST score   383
E value      1.0e-44
Match length  123
% identity    71
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
                thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                [Arabidopsis thaliana]
```

```
Seq. No.          232871
Seq. ID           LIB3272-003-P1-K1-F4
Method            BLASTX
NCBI GI           g3600030
BLAST score       299
E value           4.0e-27
Match length      106
% identity        54
NCBI Description   (AF080119) contains similarity to ankyrin repeats (Pfam:
                  ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis
                  thaliana]
```

```
Seq. No.          232872
Seq. ID           LIB3272-003-P1-K1-F6
Method            BLASTX
NCBI GI           g112925
BLAST score       169
E value           7.0e-12
Match length      108
% identity        40
NCBI Description  41-2 PROTEIN ANTIGEN PRECURSOR >gi_320938_pir_A45503 41-2
                  protein antigen precursor - Plasmodium falciparum
                  >gi_160039 (J04656) 41-2 protein antigen [Plasmodium
                  falciparum]
```

```
Seq. No.      232873
Seq. ID      LIB3272-003-P1-K1-F7
Method       BLASTX
NCBI GI      g2760084
BLAST score   223
E value      2.0e-24
Match length  92
% identity   21
NCBI Description (Y16045) leucine-rich repeat protein [Arabidopsis thaliana]
```

Seq. No.	232874
Seq. ID	LIB3272-003-P1-K1-F8
Method	BLASTX


```
Seq. No.      232879
Seq. ID      LIB3272-003-P1-K1-H1
Method       BLASTX
NCBI GI      g3123515
BLAST score   497
E value      1.0e-56
Match length  124
% identity   85
NCBI Description (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
```

```

Seq. No.                232880
Seq. ID                 LIB3272-003-P1-K1-H11
Method                  BLASTX
NCBI GI                 g2499945
BLAST score             391
E value                 6.0e-38
Match length            122
% identity               61
NCBI Description         URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                        PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                        DECARBOXYLASE >gi_1076363_pir_S46440 orotate
                        phosphoribosyltransferase (EC 2.4.2.10) /
                        orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                        Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)
                        pyrE-F [Arabidopsis thaliana]

```

```
Seq. No.      232881
Seq. ID      LIB3272-003-P1-K1-H2
Method       BLASTX
NCBI GI      g3413716
BLAST score   277
E value      1.0e-24
Match length  118
% identity    56
NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]
               >gi_3643589 (AC005395) unknown protein [Arabidopsis
               thaliana]
```

```
Seq. No.      232882
Seq. ID      LIB3272-003-P1-K1-H3
Method       BLASTX
NCBI GI      g2459417
BLAST score   404
E value      2.0e-39
Match length  139
% identity    60
NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19
               [Arabidopsis thaliana]
```

Seq. No.	232883
Seq. ID	LIB3272-003-P1-K1-H4
Method	BLASTX
NCBI GI	g3549679
BLAST score	159
E value	9.0e-11
Match length	41

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Seq. No.	232893
Seq. ID	LIB3272-004-P1-K1-A8
Method	BLASTX
NCBI GI	g2493144
BLAST score	224
E value	1.0e-18
Match length	66
% identity	73
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir_S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]


```
Seq. No.      232894
Seq. ID      LIB3272-004-P1-K1-A9
Method       BLASTX
NCBI GI      g3377797
BLAST score   468
E value      6.0e-47
Match length  127
% identity    72
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for
by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
H36046; coded for by A. thaliana cDNA T44067; coded for by
A. thaliana cDNA T14056; coded for by A. thaliana cDNA
R90691 [Ara
```

Seq. No.	232895
Seq. ID	LIB3272-004-P1-K1-B1
Method	BLASTX
NCBI GI	g4235430
BLAST score	224
E value	9.0e-34
Match length	108
% identity	75
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

```

Seq. No.          232896
Seq. ID          LIB3272-004-P1-K1-B11
Method           BLASTX
NCBI GI          g129881
BLAST score      688
E value          9.0e-73
Match length     141
% identity        93
NCBI Description  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                  (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                  (PPI-PFK) >gi_482294_pir_A36094
                  pyrophosphate--fructose 6-phosphate 1-phosphotransferase
                  (EC 2.7.1.90) alpha chain - potato (cv. Kennebec)
                  >gi_169538 (M55190) pyrophosphate-fructose 6-phosphate
                  1-phosphotransferase alpha-subunit [Solanum tuberosum]

```

Seq. No.	232897
Seq. ID	LIB3272-004-P1-K1-B12
Method	BLASTX
NCBI GI	g3158474
BLAST score	478
E value	4.0e-48
Match length	116
% identity	83
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

```
Seq. No.      232898
Seq: ID      LIB3272-004-P1-K1-B2
Method       BLASTX
NCBI GI      g3747050
BLAST score   417
```


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```
Seq. No.      232908
Seq. ID       LIB3272-004-P1-K1-C5
Method        BLASTX
NCBI GI       g4185140
BLAST score   406
E value       1.0e-39
Match length  88
% identity    91
NCBI Description (AC005724) putative small nuclear ribonucleoprotein E
                (snRNP-E) [Arabidopsis thaliana]
```



```
Seq. No.      232909
Seq. ID       LIB3272-004-P1-K1-C7
Method        BLASTX
NCBI GI       g125606
BLAST score   479
E value       3.0e-48
Match length  104
% identity    87
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
pyruvate kinase (EC 2.7.1.40) - potato
>gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
tuberosum]
```

```
Seq. No.      232910
Seq. ID       LIB3272-004-P1-K1-C8
Method        BLASTX
NCBI GI       g1107526
BLAST score   500
E value       1.0e-50
Match length  124
% identity    76
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
```

```
Seq. No.      232911
Seq. ID      LIB3272-004-P1-K1-C9
Method       BLASTX
NCBI GI      g441457
BLAST score   585
E value      1.0e-60
Match length  112
% identity    97
NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
                esculentum]
```

```

Seq. No.      232912
Seq. ID       LIB3272-004-P1-K1-D10
Method        BLASTX
NCBI GI       g1718097
BLAST score    258
E value        2.0e-22
Match length   74
% identity     64
NCBI Description  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
                  (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016
                  lysosomal membrane protein DVA41 - slime mold
                  (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]

```

```
Seq. No.          232913
Seq. ID           LIB3272-004-P1-K1-D11
Method            BLASTX
NCBI GI           g4115337
BLAST score       533
E value           1.0e-54
Match length      108
% identity        18
```



```
Seq. ID      LIB3272-005-P1-K1-F12
Method      BLASTX
NCBI GI      g1928981
BLAST score  585
E value      1.0e-60
Match length 125
% identity   63
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
oleracea var. botrytis]
```

```
Seq. No.      232984
Seq. ID      LIB3272-005-P1-K1-F3
Method       BLASTX
NCBI GI      g1173209
BLAST score   269
E value      8.0e-24
Match length  77
% identity   73
NCBI Description  40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
protein S16 protein - upland cotton
>gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit:
[Gossypium hirsutum]
```

```
Seq. No.      232985
Seq. ID       LIB3272-005-P1-K1-F5
Method        BLASTX
NCBI GI       g3641312
BLAST score    597
E value        4.0e-62
Match length   131
% identity     85
NCBI Description (AF087412) AJH2 [Arabidopsis thaliana]
```

```

Seq. No.      232986
Seq. ID       LIB3272-005-P1-K1-F7
Method        BLASTX
NCBI GI       g401329
BLAST score   159
E value       1.0e-10
Match length  110
% identity    33
NCBI Description  VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C SUBUNIT)
>gi_542836_pir_JN0907 H+-transporting ATPase (EC 3.6.1.35)
chain C, vacuolar - human >gi_37643_emb_CAA48903_ (X69151)
vacuolar proton-ATPase [Homo sapiens]
>gi_4502315_ref_NP_001686.1_pATP6D_ATPase, H+
transporting, lysosomal (vacuolar proton pump) 42kD

```

```
Seq. No.      232987
Seq. ID      LIB3272-005-P1-K1-F8
Method       BLASTX
NCBI GI      g3510254
BLAST score   596
E value      6.0e-62
Match length  138
% identity   86
NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]
```


(M88324) late embryogenesis-abundant protein [Gossypium
hirsutum] >gi_167347 (M37697) Lea5-A late
embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 233009
Seq. ID LIB3272-006-P1-K1-B10
Method BLASTX
NCBI GI g3128228
BLAST score 550
E value 1.0e-56
Match length 117
% identity 89
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis
thaliana] >gi_3337376 (AC004481) putative ribosomal protein
L18A [Arabidopsis thaliana]

Seq. No. 233010
Seq. ID LIB3272-006-P1-K1-B3
Method BLASTX
NCBI GI g4455206
BLAST score 371
E value 1.0e-35
Match length 129
% identity 60
NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis
thaliana]

Seq. No. 233011
Seq. ID LIB3272-006-P1-K1-B9
Method BLASTX
NCBI GI g543711
BLAST score 500
E value 1.0e-50
Match length 112
% identity 90
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796 pir_S30927 14-3-3
protein homolog - rice >gi_303859 dbj_BAA03711_ (D16140)
brain specific protein [Oryza sativa]

Seq. No. 233012
Seq. ID LIB3272-006-P1-K1-C2
Method BLASTX
NCBI GI g508304
BLAST score 273
E value 4.0e-24
Match length 65
% identity 78
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233013
Seq. ID LIB3272-006-P1-K1-C3
Method BLASTX
NCBI GI g167367
BLAST score 606
E value 4.0e-63
Match length 132
% identity 89

Seq. ID LIB3272-006-P1-K1-D12
 Method BLASTX
 NCBI GI g114420
 BLAST score 634
 E value 2.0e-66
 Match length 132
 % identity 94
 NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
 >gi_100882_pir_S11491 H⁺-transporting ATP synthase (EC
 3.6.1.34) beta chain, mitochondrial - maize
 >gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein
 [Zea mays] >gi_897618 (M36087) F-1-ATPase subunit 2 [Zea
 mays]

Seq. No. 233020
 Seq. ID LIB3272-006-P1-K1-D2
 Method BLASTX
 NCBI GI g1709498
 BLAST score 513
 E value 3.0e-52
 Match length 113
 % identity 81
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34. PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
 thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
 [Arabidopsis thaliana]

Seq. No. 233021
 Seq. ID LIB3272-006-P1-K1-D3
 Method BLASTX
 NCBI GI g3450842
 BLAST score 142
 E value 9.0e-09
 Match length 110
 % identity 30
 NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza
 sativa]

Seq. No. 233022
 Seq. ID LIB3272-006-P1-K1-D5
 Method BLASTX
 NCBI GI g3329368
 BLAST score 181
 E value 3.0e-21
 Match length 125
 % identity 42
 NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 233023
 Seq. ID LIB3272-006-P1-K1-D6
 Method BLASTX
 NCBI GI g1168728
 BLAST score 321
 E value 9.0e-30
 Match length 113
 % identity 52
 NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883)

E value 7.0e-43
 Match length 133
 % identity 64
 NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233039
 Seq. ID LIB3272-006-P1-K1-G1
 Method BLASTX
 NCBI GI g2191150
 BLAST score 211
 E value 2.0e-21
 Match length 88
 % identity 68
 NCBI Description (AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No. 233040
 Seq. ID LIB3272-006-P1-K1-G10
 Method BLASTX
 NCBI GI g322596
 BLAST score 376
 E value 3.0e-36
 Match length 79
 % identity 92
 NCBI Description serine/threonine protein kinase (EC 2.7.-.-) AK21 - Arabidopsis thaliana >gi_166600 (M93023) SNF1-related protein kinase [Arabidopsis thaliana]
 >gi_1742969_emb_CAA64384_ (X94757) ser/thr protein kinase [Arabidopsis thaliana]

Seq. No. 233041
 Seq. ID LIB3272-006-P1-K1-G11
 Method BLASTX
 NCBI GI g1332579
 BLAST score 514
 E value 2.0e-52
 Match length 118
 % identity 9
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 233042
 Seq. ID LIB3272-006-P1-K1-G2
 Method BLASTX
 NCBI GI g730456
 BLAST score 488
 E value 2.0e-49
 Match length 115
 % identity 75
 NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 233043
 Seq. ID LIB3272-006-P1-K1-G3
 Method BLASTX
 NCBI GI g2462762
 BLAST score 329
 E value 1.0e-30
 Match length 122

% identity 57
NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 233044
Seq. ID LIB3272-006-P1-K1-G5
Method BLASTX
NCBI GI g3059131
BLAST score 304
E value 9.0e-28
Match length 95
% identity 58
NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No. 233045
Seq. ID LIB3272-006-P1-K1-G7
Method BLASTX
NCBI GI g1332579
BLAST score 531
E value 4.0e-60
Match length 132
% identity 10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 233046
Seq. ID LIB3272-006-P1-K1-G8
Method BLASTX
NCBI GI g3860259
BLAST score 159
E value 4.0e-13
Match length 102
% identity 49
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 233047
Seq. ID LIB3272-006-P1-K1-G9
Method BLASTX
NCBI GI g2739046
BLAST score 374
E value 6.0e-36
Match length 112
% identity 62
NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No. 233048
Seq. ID LIB3272-006-P1-K1-H1
Method BLASTX
NCBI GI g3128228
BLAST score 214
E value 2.0e-17
Match length 67
% identity 67
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Method BLASTX
 NCBI GI g2764941
 BLAST score 222
 E value 3.0e-18
 Match length 72
 % identity 58
 NCBI Description (X98255) transcriptionally stimulated by gibberellins;
 expressed in meristematic region, and style [Arabidopsis
 thaliana]

Seq. No. 233055
 Seq. ID LIB3272-007-P1-K1-A1
 Method BLASTX
 NCBI GI g2160166
 BLAST score 123
 E value 1.0e-09
 Match length 66
 % identity 58
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233056
 Seq. ID LIB3272-007-P1-K1-A12
 Method BLASTX
 NCBI GI g3158376
 BLAST score 328
 E value 9.0e-31
 Match length 95
 % identity 68
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233057
 Seq. ID LIB3272-007-P1-K1-A2
 Method BLASTX
 NCBI GI g4510363
 BLAST score 249
 E value 3.0e-21
 Match length 58
 % identity 81
 NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis
 thaliana]

Seq. No. 233058
 Seq. ID LIB3272-007-P1-K1-A4
 Method BLASTX
 NCBI GI g2494905
 BLAST score 153
 E value 4.0e-10
 Match length 85
 % identity 45
 NCBI Description MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi_2132107_pir_S67174
 hypothetical protein YOR272w - yeast (Saccharomyces
 cerevisiae) >gi_1279699_emb_CAA61778_ (X89633) hypothetical
 protein [Saccharomyces cerevisiae]
 >gi_1420610_emb_CAA99497_ (Z75180) ORF YOR272w
 [Saccharomyces cerevisiae] >gi_1928989 (U92821)
 microtubule-associated protein [Saccharomyces cerevisiae]


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Seq. No.      233059
Seq. ID       LIB3272-007-P1-K1-A6
Method        BLASTX
NCBI GI       g464986
BLAST score   366
E value       3.0e-35
Match length  69
% identity    97
NCBI Description  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                >gi_421857_pir_S32674 ubiquitin--protein ligase (EC
                6.3.2.19) UBC9 - Arabidopsis thaliana
                >gi_297884_emb_CAA78714_(Z14990) ubiquitin conjugating
                enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                ubiquitin conjugating enzyme [Arabidopsis thaliana]
                >gi_600391_emb_CAA51201_(X72626) ubiquitin conjugating
                enzyme E2 [Arabidopsis thaliana]
                >gi_4455355_emb_CAB36765.1_(AL035524) ubiquitin-protein
                ligase UBC9 [Arabidopsis thaliana]

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Seq. No.          233060
Seq. ID          LIB3272-007-P1-K1-A7
Method           BLASTX
NCBI GI          g4538993
BLAST score      521
E value          3.0e-53
Match length     127
% identity       75
NCBI Description (AL049481) putative host response protein [Arabidopsis
                  thaliana]
```

```

Seq. No.      233061
Seq. ID       LIB3272-007-P1-K1-A9
Method        BLASTX
NCBI GI       g2499946
BLAST score    575
E value       2.0e-59
Match length  134
% identity    84
NCBI Description  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                  DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana
                  tabacum]

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```
Seq. No.      233062
Seq. ID      LIB3272-007-P1-K1-B1
Method       BLASTX
NCBI GI      g927575
BLAST score   405
E value      1.0e-39
Match length  90
% identity   77
NCBI Description (U12926) alpha galactosidase [Glycine max]
```

Seq. No.	233063
Seq. ID	LIB3272-007-P1-K1-B10
Method	BLASTX

NCBI GI g3914467
 BLAST score 165
 E value 1.0e-11
 Match length 79
 % identity 51
 NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
 >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana
 tabacum]

Seq. No. 233064
 Seq. ID LIB3272-007-P1-K1-B11
 Method BLASTX
 NCBI GI g4098129
 BLAST score 481
 E value 1.0e-48
 Match length 93
 % identity 94
 NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 233065
 Seq. ID LIB3272-007-P1-K1-B12
 Method BLASTX
 NCBI GI g167367
 BLAST score 354
 E value 9.0e-38
 Match length 92
 % identity 92
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 233066
 Seq. ID LIB3272-007-P1-K1-B2
 Method BLASTX
 NCBI GI g1171577
 BLAST score 401
 E value 3.0e-39
 Match length 118
 % identity 67
 NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 233067
 Seq. ID LIB3272-007-P1-K1-B3
 Method BLASTX
 NCBI GI g3738285
 BLAST score 197
 E value 3.0e-15
 Match length 80
 % identity 50
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 233068
 Seq. ID LIB3272-007-P1-K1-B6
 Method BLASTX
 NCBI GI g730241
 BLAST score 225
 E value 1.0e-18
 Match length 94
 % identity 51

NCBI GI g3881649
 BLAST score 466
 E value 1.0e-46
 Match length 88
 % identity 89
 NCBI Description (Z70757) Similarity to yeast hypothetical protein PIR accession number S52511; cDNA EST EMBL:D73067 comes from this gene; cDNA EST EMBL:D74461 comes from this gene; cDNA EST EMBL:D76044 comes from this gene; cDNA EST yk504c7.3

Seq. No. 233074
 Seq. ID LIB3272-007-P1-K1-C3
 Method BLASTX
 NCBI GI g2462762
 BLAST score 404
 E value 2.0e-39
 Match length 132
 % identity 61
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 233075
 Seq. ID LIB3272-007-P1-K1-C9
 Method BLASTX
 NCBI GI g1220180
 BLAST score 275
 E value 2.0e-24
 Match length 111
 % identity 52
 NCBI Description (Z69996) dormancy related protein [Trollius ledebourii]

Seq. No. 233076
 Seq. ID LIB3272-007-P1-K1-D10
 Method BLASTX
 NCBI GI g1946371
 BLAST score 322
 E value 4.0e-30
 Match length 82
 % identity 73
 NCBI Description (U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]

Seq. No. 233077
 Seq. ID LIB3272-007-P1-K1-D11
 Method BLASTX
 NCBI GI g113621
 BLAST score 238
 E value 2.0e-20
 Match length 54
 % identity 87
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
 >gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A cytoplasmic aldolase [Zea mays]

Seq. ID LIB3272-008-P1-K1-A3
 Method BLASTX
 NCBI GI g2149127
 BLAST score 300
 E value 2.0e-27
 Match length 108
 % identity 56
 NCBI Description (U81293) UDP-glucose:indole-3-acetate
 beta-D-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 233104
 Seq. ID LIB3272-008-P1-K1-A4
 Method BLASTX
 NCBI GI g3337356
 BLAST score 566
 E value 2.0e-58
 Match length 118
 % identity 93
 NCBI Description (AC004481) putative protein transport protein SEC61 alpha
 subunit [Arabidopsis thaliana]

Seq. No. 233105
 Seq. ID LIB3272-008-P1-K1-A7
 Method BLASTX
 NCBI GI g2245136
 BLAST score 446
 E value 2.0e-44
 Match length 120
 % identity 68
 NCBI Description (Z97344) trehalose-6-phosphate synthase homolog
 [Arabidopsis thaliana]

Seq. No. 233106
 Seq. ID LIB3272-008-P1-K1-A9
 Method BLASTX
 NCBI GI g3738301
 BLAST score 395
 E value 2.0e-38
 Match length 104
 % identity 64
 NCBI Description (AC005309) putative zinc-finger protein [Arabidopsis
 thaliana] >gi_4249397 (AC006072) putative zinc-finger
 protein (B-box zinc finger domain) [Arabidopsis thaliana]

Seq. No. 233107
 Seq. ID LIB3272-008-P1-K1-B10
 Method BLASTX
 NCBI GI g1001309
 BLAST score 216
 E value 2.0e-17
 Match length 125
 % identity 35
 NCBI Description (D64006) aspartate aminotransferase [Synechocystis sp.]

Seq. No. 233108
 Seq. ID LIB3272-008-P1-K1-B12
 Method BLASTX

Seq. No. 233113
 Seq. ID LIB3272-008-P1-K1-C11
 Method BLASTX
 NCBI GI g2244846
 BLAST score 463
 E value 2.0e-46
 Match length 118
 % identity 73
 NCBI Description (Z97337) ferredoxin [Arabidopsis thaliana]

Seq. No. 233114
 Seq. ID LIB3272-008-P1-K1-C12
 Method BLASTX
 NCBI GI g3395673
 BLAST score 450
 E value 7.0e-45
 Match length 116
 % identity 74
 NCBI Description (AB016623) RWC-3 [Oryza sativa]

Seq. No. 233115
 Seq. ID LIB3272-008-P1-K1-C2
 Method BLASTX
 NCBI GI g3024017
 BLAST score 509
 E value 9.0e-52
 Match length 99
 % identity 97
 NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No. 233116
 Seq. ID LIB3272-008-P1-K1-C4
 Method BLASTX
 NCBI GI g1518540
 BLAST score 512
 E value 4.0e-52
 Match length 108
 % identity 92
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 233117
 Seq. ID LIB3272-008-P1-K1-C5
 Method BLASTX
 NCBI GI g2129915
 BLAST score 186
 E value 4.0e-14
 Match length 72
 % identity 51
 NCBI Description ferredoxin precursor - sweet orange >gi_1360725_emb CAA87068_ (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]

Seq. No. 233118
 Seq. ID LIB3272-008-P1-K1-C8

NCBI GI g4336436
 BLAST score 493
 E value 6.0e-50
 Match length 139
 % identity 71
 NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No. 233124
 Seq. ID LIB3272-008-P1-K1-D6
 Method BLASTX
 NCBI GI g2146797
 BLAST score 549
 E value 2.0e-56
 Match length 141
 % identity 74
 NCBI Description protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
 >gi_1134968 (U41385) protein disulphide isomerase PDI
 [Ricinus communis] >gi_1587210_prf_2206331A protein
 disulfide isomerase [Ricinus communis]

Seq. No. 233125
 Seq. ID LIB3272-008-P1-K1-D7
 Method BLASTX
 NCBI GI g508304
 BLAST score 218
 E value 1.0e-17
 Match length 76
 % identity 58
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233126
 Seq. ID LIB3272-008-P1-K1-E1
 Method BLASTX
 NCBI GI g3894171
 BLAST score 496
 E value 3.0e-50
 Match length 131
 % identity 69
 NCBI Description (AC005312) putative glutathione s-transferase [Arabidopsis
 thaliana]

Seq. No. 233127
 Seq. ID LIB3272-008-P1-K1-E10
 Method BLASTX
 NCBI GI g2435604
 BLAST score 172
 E value 9.0e-27
 Match length 139
 % identity 52
 NCBI Description (AF026213) strong similarity to Saccharomyces cerevisiae
 endosomal P24A protein (SP:P32802) [Caenorhabditis elegans]

Seq. No. 233128
 Seq. ID LIB3272-008-P1-K1-E12
 Method BLASTX
 NCBI GI g2895870
 BLAST score 336

% identity 79
 NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 233144
 Seq. ID LIB3272-008-P1-K1-H11
 Method BLASTX
 NCBI GI g730463
 BLAST score 322
 E value 8.0e-30
 Match length 105
 % identity 59
 NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
 >gi_630323_pir_S44069 ribosomal protein L35a.e.c15 - yeast
 (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
 protein L37 [Saccharomyces cerevisiae]
 >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
 [Saccharomyces cerevisiae]

Seq. No. 233145
 Seq. ID LIB3272-008-P1-K1-H12
 Method BLASTX
 NCBI GI g2499946
 BLAST score 585
 E value 1.0e-60
 Match length 136
 % identity 85
 NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
 PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
 DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana
 tabacum]

Seq. No. 233146
 Seq. ID LIB3272-008-P1-K1-H2
 Method BLASTX
 NCBI GI g729470
 BLAST score 666
 E value 4.0e-70
 Match length 141
 % identity 90
 NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
 (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
 >gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2)
 precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
 (Z21493) mitochondrial formate dehydrogenase precursor
 [Solanum tuberosum]

Seq. No. 233147
 Seq. ID LIB3272-008-P1-K1-H3
 Method BLASTX
 NCBI GI g1170747
 BLAST score 353
 E value 2.0e-33
 Match length 84
 % identity 82
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
 (M88324) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167347 (M37697) Lea5-A late


```
Seq. No.      233158
Seq. ID      LIB3272-009-P1-K1-B12
Method       BLASTX
NCBI GI      g3924597
BLAST score   207
E value      2.0e-16
Match length 113
% identity    37
NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]
```

```
Seq. No.      233159
Seq. ID       LIB3272-009-P1-K1-B2
Method        BLASTX
NCBI GI       g3413473
BLAST score    281
E value       4.0e-25
Match length   116
% identity     50
NCBI Description (AJ006308) tyrosine phosphatase 1 [Glycine max]
```

```
Seq. No.      233160
Seq. ID       LIB3272-009-P1-K1-B3
Method        BLASTX
NCBI GI       g4512653
BLAST score   163
E value       2.0e-22
Match length  88
% identity    70
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.          233161
Seq. ID           LIB3272-009-P1-K1-B7
Method            BLASTX
NCBI GI           g2662343
BLAST score       471
E value           2.0e-47
Match length      106
% identity        87
NCBI Description   (D63581) EF-1 alpha [Oryza sativa]
```

```
Seq..No.      233162
Seq. ID       LIB3272-009-P1-K1-B8
Method        BLASTX
NCBI GI       g134792
BLAST score    226
E value       1.0e-18
Match length   89
% identity     52
NCBI Description MICROSOMAL SIGNAL PEPTIDASE 21 KD SUBUNIT (SPC21)
>gi_89064_pir_A34229 signal peptidase (EC 3.4.99.-) 21K
chain - dog >gi_164084 (J05069) signal peptidase 21 kDa
subunit [Canis familiaris]
```

Seq. No. 233163
Seq. ID LIB3272-009-P1-K1-C10
Method BLASTX
NCBI GI q445613

NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 233169
Seq. ID LIB3272-009-P1-K1-C9
Method BLASTX
NCBI GI g3063396
BLAST score 533
E value 1.0e-54
Match length 118
% identity 85
NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 233170
Seq. ID LIB3272-009-P1-K1-D10
Method BLASTX
NCBI GI g543905
BLAST score 694
E value 2.0e-73
Match length 133
% identity 95
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
brassinosteroid-regulated protein [Glycine max]

Seq. No. 233171
Seq. ID LIB3272-009-P1-K1-D11
Method BLASTX
NCBI GI g1703446
BLAST score 410
E value 3.0e-40
Match length 122
% identity 69
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
>gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
>gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
thaliana]

Seq. No. 233172
Seq. ID LIB3272-009-P1-K1-D12
Method BLASTX
NCBI GI g484656
BLAST score 488
E value 2.0e-49
Match length 131
% identity 71
NCBI Description monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
cucumber >gi_452165_dbj_BAA05408_ (D26392)
monodehydroascorbate reductase [Cucumis sativus]

Seq. No. 233173
Seq. ID LIB3272-009-P1-K1-D4
Method BLASTX
NCBI GI g543905
BLAST score 515
E value 2.0e-52
Match length 106
% identity 88
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)


```
Seq. No.      233179
Seq. ID      LIB3272-009-P1-K1-E11
Method       BLASTX
NCBI GI      g2160166
BLAST score   460
E value      5.0e-46
Match length  133
% identity    64
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
```

```
Seq. No.      233180
Seq. ID      LIB3272-009-P1-K1-E12
Method       BLASTX
NCBI GI      g2500399
BLAST score   503
E value      4.0e-51
Match length  114
% identity    91
NCBI Description  40S RIBOSOMAL PROTEIN S3 >gi_1836060_bbs_179561 (S83098)
               ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls,
               embryos, Peptide, 253 aa] [Ambystoma mexicanum]
```

```
Seq. No.      233181
Seq. ID      LIB3272-009-P1-K1-E5
Method       BLASTX
NCBI GI      g1657621
BLAST score   395
E value      2.0e-38
Match length  117
% identity    67
NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
              putative acyl-coA dehydrogenase [Arabidopsis thaliana]
```

```
Seq. No.          233182
Seq. ID           LIB3272-009-P1-K1-E6
Method            BLASTX
NCBI GI           g2146774
BLAST score       342
E value           1.0e-45
Match length      115
% identity        80
NCBI Description   serine acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis
                   thaliana >gi_905391 (U30298) serine acetyltransferase
                   [Arabidopsis thaliana]
```

```
Seq. No.      233183
Seq. ID      LIB3272-009-P1-K1-E7
Method       BLASTX
NCBI GI      g1332579
BLAST score   550
E value      1.0e-56
Match length  112
% identity    10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
```

Seq. No. 233184

Seq. ID	LIB3272-009-P1-K1-E9
Method	BLASTX
NCBI GI	g2739044
BLAST score	575
E value	2.0e-59
Match length	134
% identity	80
NCBI Description	(AF024651) polyphosphoinositide binding protein Sshlp [Glycine max]
Seq. No.	233185
Seq. ID	LIB3272-009-P1-K1-F10
Method	BLASTX
NCBI GI	g2739279
BLAST score	341
E value	4.0e-32
Match length	118
% identity	59
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]
Seq. No.	233186
Seq. ID	LIB3272-009-P1-K1-F5
Method	BLASTX
NCBI GI	g3046695
BLAST score	196
E value	4.0e-15
Match length	60
% identity	62
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]
Seq. No.	233187
Seq. ID	LIB3272-009-P1-K1-F7
Method	BLASTX
NCBI GI	g131385
BLAST score	555
E value	3.0e-57
Match length	134
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)
Seq. No.	233188
Seq. ID	LIB3272-009-P1-K1-F8
Method	BLASTX
NCBI GI	g1173218
BLAST score	489
E value	2.0e-49
Match length	110
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.	233189

NCBI Description (AF014375) putative JUN kinase activation domain binding protein [Medicago sativa]

Seq. No. 233211
Seq. ID LIB3272-010-P1-K1-B4
Method BLASTX
NCBI GI g3157936
BLAST score 193
E value 9.0e-15
Match length 91
% identity 45
NCBI Description (AC002131) Contains similarity to NFATc3 gb_U28807 from Mus musculus. [Arabidopsis thaliana]

Seq. No. 233212
Seq. ID LIB3272-010-P1-K1-B5
Method BLASTX
NCBI GI g1351014
BLAST score 489
E value 2.0e-49
Match length 130
% identity 76
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No. 233213
Seq. ID LIB3272-010-P1-K1-B7
Method BLASTX
NCBI GI g4469003
BLAST score 248
E value 3.0e-21
Match length 86
% identity 51
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 233214
Seq. ID LIB3272-010-P1-K1-B8
Method BLASTX
NCBI GI g1666234
BLAST score 296
E value 5.0e-27
Match length 56
% identity 100
NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No. 233215
Seq. ID LIB3272-010-P1-K1-B9
Method BLASTX
NCBI GI g2160166
BLAST score 256
E value 3.0e-22
Match length 118
% identity 54
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233216

% identity 82
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
 (M88324) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167347 (M37697) Lea5-A late
 embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 233242
 Seq. ID LIB3272-010-P1-K1-F8
 Method BLASTX
 NCBI GI g3868758
 BLAST score 230
 E value 4.0e-19
 Match length 100
 % identity 63
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 233243
 Seq. ID LIB3272-010-P1-K1-F9
 Method BLASTX
 NCBI GI g3668089
 BLAST score 212
 E value 5.0e-17
 Match length 78
 % identity 47
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 233244
 Seq. ID LIB3272-010-P1-K1-G1
 Method BLASTX
 NCBI GI g1107526
 BLAST score 511
 E value 5.0e-52
 Match length 128
 % identity 75
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 233245
 Seq. ID LIB3272-010-P1-K1-G12
 Method BLASTX
 NCBI GI g431144
 BLAST score 201
 E value 9.0e-16
 Match length 116
 % identity 47
 NCBI Description (D21824) HSP70 [Lilium longiflorum]

Seq. No. 233246
 Seq. ID LIB3272-010-P1-K1-G7
 Method BLASTX
 NCBI GI g462195
 BLAST score 385
 E value 3.0e-37
 Match length 81
 % identity 91
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 >gi_100682_pir_S21636 GOS2 protein - rice
 >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]


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% identity      80
NCBI Description (L22305) corC [Medicago sativa]

Seq. No.       233252
Seq. ID        LIB3272-011-P1-K1-A12
Method         BLASTX
NCBI GI        g2662343
BLAST score    606
E value        4.0e-63
Match length   116
% identity     100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No.       233253
Seq. ID        LIB3272-011-P1-K1-A3
Method         BLASTX
NCBI GI        g2662343
BLAST score    653
E value        1.0e-68
Match length   125
% identity     100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No.       233254
Seq. ID        LIB3272-011-P1-K1-A5
Method         BLASTX
NCBI GI        g1279588
BLAST score    405
E value        1.0e-39
Match length   114
% identity     68
NCBI Description (Z71749) glutathione S-transferase [Nicotiana
plumbaginifolia]

Seq. No.       233255
Seq. ID        LIB3272-011-P1-K1-A6
Method         BLASTX
NCBI GI        g1263291
BLAST score    565
E value        2.0e-58
Match length   117
% identity     88
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.       233256
Seq. ID        LIB3272-011-P1-K1-A8
Method         BLASTX
NCBI GI        g120669
BLAST score    229
E value        3.0e-19
Match length   54
% identity     81
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

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Seq. No.      233257
Seq. ID      LIB3272-011-P1-K1-B1
Method       BLASTX
NCBI GI      g1170747
BLAST score   338
E value      1.0e-31
Match length  79
% identity   84
NCBI Description  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
(M88324) late embryogenesis-abundant protein [Gossypium
hirsutum] >gi_167347 (M37697) LeA5-A late
embryogenesis-abundant protein [Gossypium hirsutum]
```

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Seq. No.      233258
Seq. ID      LIB3272-011-P1-K1-B11
Method       BLASTX
NCBI GI      g3033391
BLAST score   538
E value      3.0e-55
Match length  132
% identity    78
NCBI Description (AC004238) putative amino acid transporter [Arabidopsis thaliana]
```

```
Seq. No.          233259
Seq. ID           LIB3272-011-P1-K1-B2
Method            BLASTX
NCBI GI           g3953463
BLAST score       254
E value           7.0e-22
Match length      93
% identity        52
NCBI Description   (AC002328) F20N2.8 [Arabidopsis thaliana]
```

```
Seq. No.      233260
Seq. ID      LIB3272-011-P1-K1-B3
Method       BLASTX
NCBI GI      g3914605
BLAST score   348
E value      7.0e-33
Match length  117
% identity    61
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir_S39551
                ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                apple tree >gi_415852_emb_CAA79857_ (Z21794)
                ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                [Malus domestica]
```

Seq. No.	233261
Seq. ID	LIB3272-011-P1-K1-B8
Method	BLASTX
NCBI GI	g1632822
BLAST score	184
E value	6.0e-14
Match length	69

% identity 61
 NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
 (U77297) transmembrane protein [Oryza sativa]

Seq. No. 233262
 Seq. ID LIB3272-011-P1-K1-B9
 Method BLASTX
 NCBI GI g2160166
 BLAST score 328
 E value 1.0e-30
 Match length 130
 % identity 57
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233263
 Seq. ID LIB3272-011-P1-K1-C1
 Method BLASTX
 NCBI GI g1928981
 BLAST score 261
 E value 3.0e-23
 Match length 55
 % identity 93
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
 oleracea var. botrytis]

Seq. No. 233264
 Seq. ID LIB3272-011-P1-K1-C11
 Method BLASTX
 NCBI GI g2642154
 BLAST score 204
 E value 5.0e-16
 Match length 124
 % identity 44
 NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]
 >gi_3790595 (AF079186) RING-H2 finger protein RHC2a
 [Arabidopsis thaliana]

Seq. No. 233265
 Seq. ID LIB3272-011-P1-K1-C12
 Method BLASTX
 NCBI GI g3094012
 BLAST score 367
 E value 4.0e-35
 Match length 75
 % identity 87
 NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]

Seq. No. 233266
 Seq. ID LIB3272-011-P1-K1-C3
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 1.0e-14
 Match length 47
 % identity 68
 NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea
 batatas]

Seq. No. 233267
 Seq. ID LIB3272-011-P1-K1-C4
 Method BLASTX
 NCBI GI g3790569
 BLAST score 171
 E value 4.0e-12
 Match length 51
 % identity 53
 NCBI Description (AF078822) RING-H2 finger protein RHA2a [Arabidopsis thaliana]

Seq. No. 233268
 Seq. ID LIB3272-011-P1-K1-C6
 Method BLASTX
 NCBI GI g2961372
 BLAST score 647
 E value 6.0e-68
 Match length 126
 % identity 94
 NCBI Description (AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 233269
 Seq. ID LIB3272-011-P1-K1-D1
 Method BLASTX
 NCBI GI g2583134
 BLAST score 198
 E value 2.0e-15
 Match length 62
 % identity 65
 NCBI Description (AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No. 233270
 Seq. ID LIB3272-011-P1-K1-D11
 Method BLASTX
 NCBI GI g3643609
 BLAST score 434
 E value 5.0e-43
 Match length 134
 % identity 65
 NCBI Description (AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No. 233271
 Seq. ID LIB3272-011-P1-K1-D12
 Method BLASTX
 NCBI GI g4426565
 BLAST score 165
 E value 2.0e-11
 Match length 87
 % identity 40
 NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 233272

Seq. ID LIB3272-011-P1-K1-D2
 Method BLASTX
 NCBI GI g1743354
 BLAST score 416
 E value 7.0e-41
 Match length 96
 % identity 79
 NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No. 233273
 Seq. ID LIB3272-011-P1-K1-D8
 Method BLASTX
 NCBI GI g2499945
 BLAST score 416
 E value 7.0e-41
 Match length 131
 % identity 64
 NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir_S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No. 233274
 Seq. ID LIB3272-011-P1-K1-D9
 Method BLASTX
 NCBI GI g1076510
 BLAST score 555
 E value 3.0e-57
 Match length 122
 % identity 84
 NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus vulgaris]

Seq. No. 233275
 Seq. ID LIB3272-011-P1-K1-E10
 Method BLASTX
 NCBI GI g3158376
 BLAST score 431
 E value 1.0e-42
 Match length 118
 % identity 75
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233276
 Seq. ID LIB3272-011-P1-K1-E2
 Method BLASTX
 NCBI GI g401322
 BLAST score 273
 E value 4.0e-24
 Match length 67
 % identity 82
 NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_167313 (L03186) vacuolar H+-ATPase catalytic

0984016-701000

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Seq. No.      233278
Seq. ID      LIB3272-011-P1-K1-E4
Method       BLASTX
NCBI GI      g2662343
BLAST score   534
E value      8.0e-55
Match length  104
% identity    99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
```

```
Seq. No.          233280
Seq. ID          LIB3272-011-P1-K1-E9
Method           BLASTX
NCBI GI         g3063396
BLAST score      363
E value         6.0e-35
Match length     76
% identity       88
NCBI Description (AB012947) vcCyP [Vicia faba]
```

Seq. No. 233282
Seq. ID LIB3272-011-P1-K1-F10
Method BLASTX
NCBI GI g3094012


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BLAST score      369
E value         3.0e-36
Match length    96
% identity      82
NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
```

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Seq. No.      233283
Seq. ID      LIB3272-011-P1-K1-F12
Method       BLASTX
NCBI GI      g1076621
BLAST score   560
E value      9.0e-58
Match length  119
% identity    85
NCBI Description  cytochrome b5.- common tobacco >gi_296386_emb_CAA50575_
                  (X71441) cytochrome b5 [Nicotiana tabacum]
```

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Seq. No.                233284
Seq. ID                 LIB3272-011-P1-K1-F3
Method                  BLASTX
NCBI GI                 g464986
BLAST score             256
E value                 2.0e-22
Match length            54
% identity              89
NCBI Description        UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                        LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                        >gi_421857_pir_S32674 ubiquitin--protein ligase (EC
                        6.3.2.19) UBC9 - Arabidopsis thaliana
                        >gi_297884_emb_CAA78714_(Z14990) ubiquitin conjugating
                        enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                        ubiquitin conjugating enzyme [Arabidopsis thaliana]
                        >gi_600391_emb_CAA51201_(X72626) ubiquitin conjugating
                        enzyme E2 [Arabidopsis thaliana]
                        >gi_4455355_emb_CAB36765.1_(AL035524) ubiquitin-protein
                        ligase UBC9 [Arabidopsis thaliana]

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```
Seq. No.      233285
Seq. ID      LIB3272-011-P1-K1-F5
Method       BLASTX
NCBI GI      g1703446
BLAST score   386
E value      2.0e-37
Match length  122
% identity    65
NCBI Description  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                >gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
                >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
                thaliana]
```

```
Seq. No.      233286
Seq. ID       LIB3272-011-P1-K1-F6
Method        BLASTX
NCBI GI       g133940
BLAST score    140
E value       1.0e-08
Match length   39
```


NCBI GI g122085
 BLAST score 493
 E value 6.0e-50
 Match length 115
 % identity 87
 NCBI Description HISTONE H3 >gi_81641_pir_S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir_S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir_S57626 histone H3 - maize >gi_20251_emb_CAA31969_(X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_(X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493_(M36658) histone H3 (H3C3) [Zea mays] >gi_168495_(M13378) histone H3 [Zea mays] >gi_168497_(M13379) histone H3 [Zea mays] >gi_168506_(M35388) histone H3 [Zea mays] >gi_169655_(M77493) histone H3 [Petroselinum crispum] >gi_169657_(M77494) histone H3 [Petroselinum crispum] >gi_169659_(M77495) histone H3 [Petroselinum crispum] >gi_387565_(M17130) histone H3 [Arabidopsis thaliana] >gi_387567_(M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_(X84377) histone 3 [Zea mays] >gi_1040764_(M35387) histone H3 [Arabidopsis thaliana] >gi_1314779_(U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_(X82414) Histone H3 [Asparagus officinalis] >gi_1667592_(U77296) histone 3. [Oryza sativa] >gi_3249101_(AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf_1303352A histone H3 [Helicoverpa zea] >gi_225839_prf_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 233292
 Seq. ID LIB3272-011-P1-K1-H1
 Method BLASTX
 NCBI GI g120669
 BLAST score 576
 E value 1.0e-59
 Match length 114
 % identity 95
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_(X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 233293
 Seq. ID LIB3272-011-P1-K1-H2
 Method BLASTX
 NCBI GI g3759184
 BLAST score 283
 E value 3.0e-25
 Match length 135
 % identity 50
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 233294
 Seq. ID LIB3272-011-P1-K1-H3
 Method BLASTX

NCBI GI g2347098
 BLAST score 340
 E value 6.0e-32
 Match length 69
 % identity 90
 NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
 >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
 protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 233295
 Seq. ID LIB3272-011-P1-K1-H6
 Method BLASTX
 NCBI GI g3894178
 BLAST score 269
 E value 1.0e-23
 Match length 57
 % identity 86
 NCBI Description (AC005312) putative nucleic acid binding protein
 [Arabidopsis thaliana]

Seq. No. 233296
 Seq. ID LIB3272-011-P1-K1-H7
 Method BLASTX
 NCBI GI g1170748
 BLAST score 337
 E value 1.0e-31
 Match length 79
 % identity 84
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-D >gi_167349
 (M88323) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167351 (L01102) late embryogenesis-abundant
 protein [Gossypium hirsutum]

Seq. No. 233297
 Seq. ID LIB3272-012-P1-K1-A10
 Method BLASTX
 NCBI GI g508304
 BLAST score 261
 E value 9.0e-23
 Match length 61
 % identity 80
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233298
 Seq. ID LIB3272-012-P1-K1-A11
 Method BLASTX
 NCBI GI g4510373
 BLAST score 291
 E value 3.0e-26
 Match length 109
 % identity 56
 NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis
 thaliana]

Seq. No. 233299
 Seq. ID LIB3272-012-P1-K1-A12
 Method BLASTX

Method BLASTX
NCBI GI g1769903
BLAST score 376
E value 3.0e-36
Match length 118
% identity 59
NCBI Description (X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No. 233305
Seq. ID LIB3272-012-P1-K1-C11
Method BLASTX
NCBI GI g1666234
BLAST score 276
E value 5.0e-32
Match length 87
% identity 79
NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No. 233306
Seq. ID LIB3272-012-P1-K1-C3
Method BLASTX
NCBI GI g2388575
BLAST score 261
E value 1.0e-22
Match length 130
% identity 40
NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 233307
Seq. ID LIB3272-012-P1-K1-C4
Method BLASTX
NCBI GI g4335763
BLAST score 251
E value 2.0e-21
Match length 90
% identity 50
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 233308
Seq. ID LIB3272-012-P1-K1-C6
Method BLASTX
NCBI GI g3941543
BLAST score 193
E value 1.0e-14
Match length 54
% identity 70
NCBI Description (AF069497) pelota [Arabidopsis thaliana]
>gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
[Arabidopsis thaliana]

Seq. No. 233309
Seq. ID LIB3272-012-P1-K1-C7
Method BLASTX
NCBI GI g3290020
BLAST score 518
E value 8.0e-53

Method BLASTX
 NCBI GI g122770
 BLAST score 491
 E value 1.0e-49
 Match length 126
 % identity 81
 NCBI Description HEMOGLOBIN II >gi_99509_pir_S13378 hemoglobin II - swamp oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina glauca]

Seq. No. 233336
 Seq. ID LIB3272-012-P1-K1-H11
 Method BLASTX
 NCBI GI g2463569
 BLAST score 466
 E value 7.0e-48
 Match length 111
 % identity 82
 NCBI Description (AB007503) squalene synthase [Glycine max]

Seq. No. 233337
 Seq. ID LIB3272-012-P1-K1-H3
 Method BLASTX
 NCBI GI g132853
 BLAST score 279
 E value 3.0e-37
 Match length 122
 % identity 63
 NCBI Description 60S RIBOSOMAL PROTEIN L2 >gi_71076_pir_R5D02 ribosomal protein L8.e - slime mold (Dictyostelium discoideum) >gi_7355_emb_CAA33741_ (X15710) ribosomal protein L2 (AA 1-237) [Dictyostelium discoideum]

Seq. No. 233338
 Seq. ID LIB3272-012-P1-K1-H6
 Method BLASTX
 NCBI GI g3337367
 BLAST score 202
 E value 9.0e-16
 Match length 95
 % identity 45
 NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233339
 Seq. ID LIB3272-012-P1-K1-H9
 Method BLASTX
 NCBI GI g224293
 BLAST score 410
 E value 3.0e-40
 Match length 82
 % identity 100
 NCBI Description histone H4 [Triticum aestivum]

Seq. No. 233340
 Seq. ID LIB3272-013-P1-K1-A1
 Method BLASTX
 NCBI GI g2462762


```

BLAST score      193
E value          8.0e-15
Match length     100
% identity       47
NCBI Description (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family) [Arabidopsis thaliana]

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Seq. No.      233341
Seq. ID      LIB3272-013-P1-K1-A12
Method       BLASTX
NCBI GI      g2129759
BLAST score   493
E value      6.0e-50
Match length  128
% identity    78
NCBI Description  UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana
                >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate
                glucose epimerase [Arabidopsis thaliana]
```

```
Seq. No.      233342
Seq. ID      LIB3272-013-P1-K1-A2
Method       BLASTX
NCBI GI      g3204106
BLAST score   123
E value      9.0e-11
Match length  66
% identity    58
NCBI Description (AJ006763) putative beta-amylase [Cicer arietinum]
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Seq. No.      233343
Seq. ID      LIB3272-013-P1-K1-A3
Method       BLASTX
NCBI GI      g2924509
BLAST score   274
E value      3.0e-24
Match length  95
% identity    55
NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis
                thaliana]
```

```
Seq. No.      233344
Seq. ID      LIB3272-013-P1-K1-A6
Method       BLASTX
NCBI GI      g481236
BLAST score   246
E value      5.0e-21
Match length  60
% identity    80
NCBI Description  hypothetical protein - Madagascar periwinkle
                  >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide
                  [Catharanthus roseus]
```

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Seq. No.      233345
Seq. ID       LIB3272-013-P1-K1-A7
Method        BLASTX
NCBI GI       g2462753
BLAST score   172
```


E value 2.0e-12
 Match length 43
 % identity 72
 NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 233346
 Seq. ID LIB3272-013-P1-K1-A8
 Method BLASTX
 NCBI GI g3492806
 BLAST score 204
 E value 1.0e-17
 Match length 107
 % identity 55
 NCBI Description (AJ225045) adventitious rooting related oxygenase [Malus domestica]

Seq. No. 233347
 Seq. ID LIB3272-013-P1-K1-A9
 Method BLASTX
 NCBI GI g2462753
 BLAST score 168
 E value 7.0e-12
 Match length 43
 % identity 72
 NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 233348
 Seq. ID LIB3272-013-P1-K1-B1
 Method BLASTX
 NCBI GI g3252868
 BLAST score 224
 E value 2.0e-18
 Match length 77
 % identity 53
 NCBI Description (AF033536) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 233349
 Seq. ID LIB3272-013-P1-K1-B10
 Method BLASTX
 NCBI GI g4567301
 BLAST score 179
 E value 3.0e-13
 Match length 54
 % identity 63
 NCBI Description (AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No. 233350
 Seq. ID LIB3272-013-P1-K1-B11
 Method BLASTX
 NCBI GI g1172873
 BLAST score 536
 E value 5.0e-55
 Match length 128
 % identity 70
 NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir_JN0719

drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - *Arabidopsis thaliana* >gi_435619_dbj_BAA02374_ (D13043) thiol protease [*Arabidopsis thaliana*]

```
Seq. No.      233351
Seq. ID      LIB3272-013-P1-K1-B12
Method       BLASTX
NCBI GI      g2213852
BLAST score   200
E value      1.0e-15
Match length  87
% identity    52
NCBI Description (AF003007) VVTL1 [Vitis vinifera]
```

```
Seq. No.      233352
Seq. ID      LIB3272-013-P1-K1-B3
Method       BLASTX
NCBI GI      g3868758
BLAST score   417
E value      5.0e-41
Match length  100
% identity   76
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
```

Seq. No.	233353
Seq. ID	LIB3272-013-P1-K1-B4
Method	BLASTX
NCBI GI	g2739365
BLAST score	540
E value	2.0e-55
Match length	119
% identity	80
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

```
Seq. No.      233354
Seq. ID      LIB3272-013-P1-K1-B6
Method       BLASTX
NCBI GI      g4006854
BLAST score   379
E value      1.0e-36
Match length  118
% identity    65
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
```

```
Seq. No. 233355
Seq. ID LIB3272-013-P1-K1-B9
Method BLASTX
NCBI GI g113621
BLAST score 483
E value 9.0e-49
Match length 108
% identity 88
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
```



```
Seq. No.      233361
Seq. ID      LIB3272-013-P1-K1-C8
Method       BLASTX
NCBI GI      g400650
BLAST score   183
E value      1.0e-13
Match length  93
% identity   42
NCBI Description  NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX
I-13KD-B) (CI-13KD-B) (B13) >gi_346535_pir_S28244 NADH
dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 -
bovine >gi_238_emb_CAA44903_ (X63218) NADH dehydrogenase
[Bos taurus]
```

```
Seq. No.      233362
Seq. ID      LIB3272-013-P1-K1-C9
Method       BLASTX
NCBI GI      g1658197
BLAST score   584
E value      1.0e-60
Match length  122
% identity    87
NCBI Description (U74630) calreticulin [Ricinus communis] >gi_1763297
                (U74631) calreticulin [Ricinus communis]
```

```
Seq. No.      233363
Seq. ID      LIB3272-013-P1-K1-D1
Method       BLASTX
NCBI GI      g3094012
BLAST score   360
E value      2.0e-34
Match length  75
% identity    85
NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
```

```
Seq. No.          233364
Seq. ID          LIB3272-013-P1-K1-D10
Method           BLASTX
NCBI GI          g2493130
BLAST score       625
E value          2.0e-65
Match length     121
% identity        100
NCBI Description  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B
                  SUBUNIT) >gi_459200 (U07053) vacuolar H+-ATPase subunit B
                  [Gossypium hirsutum]
```

```
Seq. No.      233365
Seq. ID      LIB3272-013-P1-K1-D11
Method       BLASTX
NCBI GI      g4323298
BLAST score   228
E value      7.0e-19
Match length  107
% identity    46
NCBI Description (AF099096) pulvinus outward-rectifying channel for
potassium SPOCK1 [Samanea saman]
```


leucine aminopeptidase [Arabidopsis thaliana]

Seq. No. 233371
 Seq. ID LIB3272-013-P1-K1-E11
 Method BLASTX
 NCBI GI g2708484
 BLAST score 148
 E value 2.0e-09
 Match length 115
 % identity 38
 NCBI Description (U79557) IAA24 [Arabidopsis thaliana]

Seq. No. 233372
 Seq. ID LIB3272-013-P1-K1-E12
 Method BLASTX
 NCBI GI g122770
 BLAST score 341
 E value 2.0e-37
 Match length 112
 % identity 75
 NCBI Description HEMOGLOBIN II >gi_99509_pir_S13378 hemoglobin II - swamp
 oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina
 glauca]

Seq. No. 233373
 Seq. ID LIB3272-013-P1-K1-E2
 Method BLASTX
 NCBI GI g1166450
 BLAST score 321
 E value 9.0e-30
 Match length 71
 % identity 82
 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]

Seq. No. 233374
 Seq. ID LIB3272-013-P1-K1-E3
 Method BLASTX
 NCBI GI g2497538
 BLAST score 396
 E value 1.0e-38
 Match length 122
 % identity 71
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)
 pyruvate kinase [Glycine max]

Seq. No. 233375
 Seq. ID LIB3272-013-P1-K1-E4
 Method BLASTX
 NCBI GI g416639
 BLAST score 154
 E value 3.0e-10
 Match length 76
 % identity 46
 NCBI Description INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG2
 >gi_287564_dbj_BAA03307_ (D14411) ORF [Vigna radiata]

Seq. No. 233376

NCBI Description (Z97336) CCAAT-binding transcription factor subunit
A(CBF-A) [Arabidopsis thaliana]

Seq. No. 233391
Seq. ID LIB3272-014-P1-K1-A1
Method BLASTX
NCBI GI g3334405
BLAST score 513
E value 2.0e-52
Match length 108
% identity 97
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
>gi_2267583 (AF009338) vacuolar H⁺-ATPase subunit E
[Gossypium hirsutum]

Seq. No. 233392
Seq. ID LIB3272-014-P1-K1-A10
Method BLASTX
NCBI GI g2347199
BLAST score 642
E value 2.0e-67
Match length 137
% identity 82
NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 233393
Seq. ID LIB3272-014-P1-K1-A11
Method BLASTX
NCBI GI g508304
BLAST score 241
E value 2.0e-20
Match length 82
% identity 57
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233394
Seq. ID LIB3272-014-P1-K1-A2
Method BLASTX
NCBI GI g3643594
BLAST score 458
E value 8.0e-46
Match length 125
% identity 74
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 233395
Seq. ID LIB3272-014-P1-K1-A4
Method BLASTX
NCBI GI g1709970
BLAST score 446
E value 2.0e-44
Match length 121
% identity 74
NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 233396
Seq. ID LIB3272-014-P1-K1-A5

NCBI Description (AB007503) squalene synthase [Glycine max]

Seq. No. 233427
Seq. ID LIB3272-014-P1-K1-E5
Method BLASTX
NCBI GI g553107
BLAST score 399
E value 7.0e-39
Match length 114
% identity 68
NCBI Description (L04967) triosephosphate isomerase [Oryza sativa]

Seq. No. 233428
Seq. ID LIB3272-014-P1-K1-E7
Method BLASTX
NCBI GI g2160166
BLAST score 304
E value 1.0e-27
Match length 128
% identity 55
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233429
Seq. ID LIB3272-014-P1-K1-E8
Method BLASTX
NCBI GI g4056494
BLAST score 306
E value 5.0e-28
Match length 100
% identity 61
NCBI Description (AC005896) putative protein translocase [Arabidopsis thaliana]

Seq. No. 233430
Seq. ID LIB3272-014-P1-K1-E9
Method BLASTX
NCBI GI g4467159
BLAST score 443
E value 5.0e-44
Match length 132
% identity 67
NCBI Description (AL035540) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233431
Seq. ID LIB3272-014-P1-K1-F1
Method BLASTX
NCBI GI g3334147
BLAST score 439
E value 1.0e-43
Match length 122
% identity 70
NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No. 233432
Seq. ID LIB3272-014-P1-K1-F10
Method BLASTX

NCBI Description (AC006201) putative peptide methionine sulfoxide reductase [Arabidopsis thaliana]

Seq. No. 233438
Seq. ID LIB3272-014-P1-K1-F9
Method BLASTX
NCBI GI g2500378
BLAST score 434
E value 5.0e-43
Match length 95
% identity 83
NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. 233439
Seq. ID LIB3272-014-P1-K1-G1
Method BLASTX
NCBI GI g1928981
BLAST score 583
E value 2.0e-60
Match length 122
% identity 63
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 233440
Seq. ID LIB3272-014-P1-K1-G10
Method BLASTX
NCBI GI g3980415
BLAST score 396
E value 2.0e-38
Match length 120
% identity 62
NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No. 233441
Seq. ID LIB3272-014-P1-K1-G2
Method BLASTX
NCBI GI g629483
BLAST score 338
E value 1.0e-31
Match length 122
% identity 56
NCBI Description gene 1-Sc3 protein - European white birch
>gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
>gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula pendula]

Seq. No. 233442
Seq. ID LIB3272-014-P1-K1-G4
Method BLASTX
NCBI GI g2244847
BLAST score 311
E value 1.0e-28
Match length 119
% identity 55
NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog

0968-0101

```
Seq. No.      233444
Seq. ID      LIB3272-014-P1-K1-G7
Method       BLASTX
NCBI GI      g4567251
BLAST score   309
E value      2.0e-28
Match length  80
% identity    66
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      233446
Seq. ID      LIB3272-014-P1-K1-H2
Method       BLASTX
NCBI GI      g117765
BLAST score   230
E value      5.0e-19
Match length  67
% identity    64
NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC13III)
                >gi_21439_emb_CAA44055_(X62124) cytochrome c1 [Solanum
                tuberosum]
```

Seq. No. 233448

Method BLASTX
 NCBI GI g2262173
 BLAST score 376
 E value 3.0e-36
 Match length 137
 % identity 57
 NCBI Description (AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No. 233459
 Seq. ID LIB3272-015-P1-K1-B6
 Method BLASTX
 NCBI GI g2961372
 BLAST score 355
 E value 9.0e-47
 Match length 114
 % identity 85
 NCBI Description (AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 233460
 Seq. ID LIB3272-015-P1-K1-B7
 Method BLASTX
 NCBI GI g267069
 BLAST score 382
 E value 4.0e-37
 Match length 72
 % identity 96
 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 233461
 Seq. ID LIB3272-015-P1-K1-B9
 Method BLASTX
 NCBI GI g1703108
 BLAST score 490
 E value 1.0e-49
 Match length 90
 % identity 100
 NCBI Description ACTIN 2/7 >gi_2129525_pir_S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir_S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No. 233462
 Seq. ID LIB3272-015-P1-K1-C10
 Method BLASTX
 NCBI GI g3193298
 BLAST score 364
 E value 9.0e-35
 Match length 110
 % identity 63
 NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]

00664016-101000

Seq. No. 233463
Seq. ID LIB3272-015-P1-K1-C2
Method BLASTX
NCBI GI g3158376
BLAST score 165
E value 6.0e-21
Match length 106
% identity 55
NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233464
Seq. ID LIB3272-015-P1-K1-C6
Method BLASTX
NCBI GI g629483
BLAST score 334
E value 3.0e-31
Match length 122
% identity 55
NCBI Description gene 1-Sc3 protein - European white birch
>gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
>gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula
pendula]

Seq. No. 233465
Seq. ID LIB3272-015-P1-K1-C7
Method BLASTX
NCBI GI g2231034
BLAST score 576
E value 1.0e-59
Match length 125
% identity 87
NCBI Description (Y12785) MAP kinase I [Petroselinum crispum]

Seq. No. 233466
Seq. ID LIB3272-015-P1-K1-C9
Method BLASTX
NCBI GI g3482918
BLAST score 589
E value 4.0e-61
Match length 130
% identity 89
NCBI Description (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
thaliana]

Seq. No. 233467
Seq. ID LIB3272-015-P1-K1-D1
Method BLASTX
NCBI GI g2129605
BLAST score 290
E value 2.0e-26
Match length 65
% identity 85
NCBI Description GTP-binding protein 2 - Arabidopsis thaliana
>gi_2129702_pir_S71585 Rab2 homolog GTP-binding protein
ATGB2 - Arabidopsis thaliana >gi_1184983 (U46925) ATGB2
[Arabidopsis thaliana] >gi_3805852_emb_CAA21472_ (AL031986)

0966-0766 = 202003

Seq. No.	233473
Seq. ID	LIB3272-015-P1-K1-D6

Method BLASTX
 NCBI GI g416649
 BLAST score 367
 E value 4.0e-35
 Match length 111
 % identity 63
 NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT1/PCNT110) >gi_100303_pir_S16267 auxin-induced protein (clone pGNT1) - common tobacco >gi_19789_emb_CAA39709_ (X56268) auxin-induced protein [Nicotiana tabacum] >gi_19795_emb_CAA39705_ (X56264) auxin-induced protein [Nicotiana tabacum]

Seq. No. 233474
 Seq. ID LIB3272-015-P1-K1-D9
 Method BLASTX
 NCBI GI g464986
 BLAST score 577
 E value 9.0e-60
 Match length 108
 % identity 99
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 233475
 Seq. ID LIB3272-015-P1-K1-E1
 Method BLASTX
 NCBI GI g2129889
 BLAST score 524
 E value 1.0e-53
 Match length 102
 % identity 97
 NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea

Seq. No. 233476
 Seq. ID LIB3272-015-P1-K1-E11
 Method BLASTX
 NCBI GI g2970654
 BLAST score 321
 E value 1.0e-29
 Match length 111
 % identity 66
 NCBI Description (AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No. 233477
 Seq. ID LIB3272-015-P1-K1-E4
 Method BLASTX

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana
tabacum]

Seq. No. 233522
Seq. ID LIB3272-016-P1-K1-C7
Method BLASTX
NCBI GI g2209384
BLAST score 421
E value 2.0e-41
Match length 96
% identity 88
NCBI Description (AF008441) glutathione reductase [Brassica rapa]

Seq. No. 233523
Seq. ID LIB3272-016-P1-K1-D1
Method BLASTX
NCBI GI g1709498
BLAST score 490
E value 1.0e-49
Match length 107
% identity 82
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
>gi_1362001_pir_S57524.osmotin precursor - Arabidopsis
thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
[Arabidopsis thaliana]

Seq. No. 233524
Seq. ID LIB3272-016-P1-K1-D11
Method BLASTX
NCBI GI g464365
BLAST score 492
E value 8.0e-50
Match length 128
% identity 76
NCBI Description PEROXIDASE P7 >gi_66306_pir_OPNB7 peroxidase (EC 1.11.1.7)
- turnip

Seq. No. 233525
Seq. ID LIB3272-016-P1-K1-D4
Method BLASTX
NCBI GI g3885884
BLAST score 449
E value 1.0e-44
Match length 101
% identity 86
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 233526
Seq. ID LIB3272-016-P1-K1-D6
Method BLASTX
NCBI GI g1170747
BLAST score 285
E value 1.0e-25
Match length 70
% identity 81
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345

09634016 101000

```
Seq. No.      233528
Seq. ID       LIB3272-016-P1-K1-E12
Method        BLASTX
NCBI GI       g1449179
BLAST score   591
E value       2.0e-61
Match length  127
% identity    93
NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein
[Nicotiana tabacum]
```

```
Seq. No.      233530
Seq. ID      LIB3272-016-P1-K1-E3
Method       BLASTX
NCBI GI      g4519264
BLAST score   630
E value      5.0e-66
Match length  128
% identity    98
NCBI Description (AB024277) vacuolar H+-ATPase B subunit [Citrus unshiu]
```

33703

0903401E 101000

```
Seq. No.      233538
Seq. ID      LIB3272-016-P1-K1-G10
Method       BLASTX
NCBI GI      g951427
BLAST score   479
E value      3.0e-48
Match length  127
% identity    70
NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]
```

```
Seq. No.      233540
Seq. ID       LIB3272-Q16-P1-K1-G7
Method        BLASTX
NCBI GI       g3413717
BLAST score    399
E value        6.0e-39
Match length   87
% identity     82
NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]
                >gi_3643590 (AC005395) unknown protein [Arabidopsis
                thaliana]
```

33705

Match length 71
 % identity 58
 NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 233547
 Seq. ID LIB3272-016-P1-K1-H7
 Method BLASTX
 NCBI GI g1245182
 BLAST score 461
 E value 3.0e-46
 Match length 110
 % identity 77
 NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No. 233548
 Seq. ID LIB3272-017-P1-K1-A1
 Method BLASTX
 NCBI GI g4263776
 BLAST score 326
 E value 3.0e-30
 Match length 142
 % identity 55
 NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]
 >gi_4510390_gb_AAD21478.1_ (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 233549
 Seq. ID LIB3272-017-P1-K1-A11
 Method BLASTX
 NCBI GI g462195
 BLAST score 434
 E value 5.0e-43
 Match length 90
 % identity 93
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 >gi_100682_pir_S21636 GOS2 protein - rice
 >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
 >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 233550
 Seq. ID LIB3272-017-P1-K1-A5
 Method BLASTX
 NCBI GI g1717949
 BLAST score 314
 E value 6.0e-29
 Match length 74
 % identity 77
 NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1
 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1)
 >gi_100375_pir_B41607 ubiquinol--cytochrome-c reductase
 (EC 1.10.2.2) iron-sulfur protein precursor - common
 tobacco (fragment) >gi_170322 (M77225) Rieske Fe-S protein [Nicotiana tabacum]

Seq. No. 233551
 Seq. ID LIB3272-017-P1-K1-A9

Method	BLASTX
NCBI GI	g2739168
BLAST score	493
E value	7.0e-50
Match length	135
% identity	67
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]
Seq. No.	233552
Seq. ID	LIB3272-017-P1-K1-B1
Method	BLASTX
NCBI GI	g586076
BLAST score	654
E value	9.0e-69
Match length	122
% identity	98
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir_S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]
Seq. No.	233553
Seq. ID	LIB3272-017-P1-K1-B10
Method	BLASTX
NCBI GI	g3901014
BLAST score	217
E value	1.0e-17
Match length	56
% identity	71
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]
Seq. No.	233554
Seq. ID	LIB3272-017-P1-K1-B11
Method	BLASTX
NCBI GI	g729672
BLAST score	153
E value	2.0e-21
Match length	94
% identity	59
NCBI Description	HISTONE H2A >gi_323111_pir_A45564 histone 2A - Plasmodium falciparum >gi_160319 (M86865) H2A [Plasmodium falciparum]
Seq. No.	233555
Seq. ID	LIB3272-017-P1-K1-B4
Method	BLASTX
NCBI GI	g3687243
BLAST score	245
E value	8.0e-21
Match length	61
% identity	79
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]
Seq. No.	233556
Seq. ID	LIB3272-017-P1-K1-B6
Method	BLASTX

% identity	50
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]
Seq. No.	233562
Seq. ID	LIB3272-017-P1-K1-C4
Method	BLASTX
NCBI GI	g441457
BLAST score	634
E value	2.0e-66
Match length	119
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]
Seq. No.	233563
Seq. ID	LIB3272-017-P1-K1-C5
Method	BLASTX
NCBI GI	g4105798
BLAST score	93
E value	5.0e-09
Match length	58
% identity	59
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.	233564
Seq. ID	LIB3272-017-P1-K1-C6
Method	BLASTX
NCBI GI	g3901014
BLAST score	235
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]
Seq. No.	233565
Seq. ID	LIB3272-017-P1-K1-C7
Method	BLASTX
NCBI GI	g2909783
BLAST score	413
E value	1.0e-40
Match length	138
% identity	63
NCBI Description	(AF020289) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]
Seq. No.	233566
Seq. ID	LIB3272-017-P1-K1-D1
Method	BLASTX
NCBI GI	g3747050
BLAST score	425
E value	6.0e-42
Match length	106
% identity	77
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]
Seq. No.	233567

Seq. ID LIB3272-017-P1-K1-D10
 Method BLASTX
 NCBI GI g1684857
 BLAST score 623
 E value 4.0e-65
 Match length 126
 % identity 40
 NCBI Description (U77940) polyubiquitin [Phaseolus vulgaris]

Seq. No. 233568
 Seq. ID LIB3272-017-P1-K1-D11
 Method BLASTX
 NCBI GI g3080440
 BLAST score 151
 E value 8.0e-10
 Match length 53
 % identity 58
 NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233569
 Seq. ID LIB3272-017-P1-K1-D12
 Method BLASTX
 NCBI GI g2160166
 BLAST score 332
 E value 5.0e-31
 Match length 131
 % identity 57
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233570
 Seq. ID LIB3272-017-P1-K1-D5
 Method BLASTX
 NCBI GI g267131
 BLAST score 186
 E value 7.0e-14
 Match length 86
 % identity 16
 NCBI Description NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN)
 >gi_423120_pir_A46174 RNA-binding protein TIAR - human
 >gi_189310 (M96954) nucleolysin TIAR [Homo sapiens]
 >gi_4507499_ref NP_003243.1 pTIAL1 TIA1 cytotoxic
 granule-associated RNA-binding protein-like

Seq. No. 233571
 Seq. ID LIB3272-017-P1-K1-D6
 Method BLASTX
 NCBI GI g4056469
 BLAST score 581
 E value 3.0e-60
 Match length 113
 % identity 100
 NCBI Description (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
 factor from Arabidopsis thaliana. ESTs gb_Z25826,
 gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
 gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and
 gb_Z25043 come from t

NCBI GI g508304
 BLAST score 216
 E value 2.0e-17
 Match length 75
 % identity 59
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233613
 Seq. ID LIB3272-018-P1-K1-B12
 Method BLASTX
 NCBI GI g3901014
 BLAST score 235
 E value 1.0e-19
 Match length 55
 % identity 76
 NCBI Description (AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No. 233614
 Seq. ID LIB3272-018-P1-K1-B2
 Method BLASTX
 NCBI GI g2507442
 BLAST score 166
 E value 4.0e-12
 Match length 42
 % identity 74
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1419685_emb_CAA67207_ (X98618) TCTP-like protein
 [Medicago sativa]

Seq. No. 233615
 Seq. ID LIB3272-018-P1-K1-B3
 Method BLASTX
 NCBI GI g1944403
 BLAST score 468
 E value 6.0e-47
 Match length 127
 % identity 73
 NCBI Description (D86590) cinnamyl alcohol dehydrogenase [Zinnia elegans]

Seq. No. 233616
 Seq. ID LIB3272-018-P1-K1-B4
 Method BLASTX
 NCBI GI g2695711
 BLAST score 526
 E value 1.0e-53
 Match length 118
 % identity 81
 NCBI Description (AJ001370) cytochrome b5 [Olea europaea]

Seq. No. 233617
 Seq. ID LIB3272-018-P1-K1-B5
 Method BLASTX
 NCBI GI g3176691
 BLAST score 395
 E value 2.0e-38
 Match length 121

% identity 36
 NCBI Description (AC003671) Contains homology to serine/threonine protein kinase gb_X99618 from Mycobacterium tuberculosis. ESTs gb_F14403, gb_F14404, and gb_N96730 come from this gene. [Arabidopsis thaliana]

Seq. No. 233618
 Seq. ID LIB3272-018-P1-K1-B7
 Method BLASTX
 NCBI GI g4262174
 BLAST score 236
 E value 2.0e-20
 Match length 50
 % identity 80
 NCBI Description (AC005508) 9058 [Arabidopsis thaliana]

Seq. No. 233619
 Seq. ID LIB3272-018-P1-K1-B8
 Method BLASTX
 NCBI GI g3694872
 BLAST score 384
 E value 2.0e-37
 Match length 80
 % identity 88
 NCBI Description (AF092547) profilin [Ricinus communis]

Seq. No. 233620
 Seq. ID LIB3272-018-P1-K1-B9
 Method BLASTX
 NCBI GI g2677828
 BLAST score 456
 E value 1.0e-45
 Match length 118
 % identity 70
 NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No. 233621
 Seq. ID LIB3272-018-P1-K1-C1
 Method BLASTX
 NCBI GI g2459417
 BLAST score 382
 E value 7.0e-37
 Match length 143
 % identity 56
 NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No. 233622
 Seq. ID LIB3272-018-P1-K1-C11
 Method BLASTX
 NCBI GI g1665867
 BLAST score 456
 E value 1.0e-45
 Match length 117
 % identity 70
 NCBI Description (Y09123) aspartic proteinase [Centaurea calcitrapa]


```
Seq. No.      233623
Seq. ID       LIB3272-018-P1-K1-C12
Method        BLASTX
NCBI GI       g4098321
BLAST score    639
E value       4.0e-67
Match length   124
% identity     98
NCBI Description (U76745) beta-tubulin 2 [Triticum aestivum]
```

```
Seq. No.          233624
Seq. ID           LIB3272-018-P1-K1-C2
Method            BLASTX
NCBI GI           g2244750
BLAST score       710
E value           2.0e-75
Match length      139
% identity        98
NCBI Description   [Z97335] adenosylhomocysteinase [Arabidopsis thaliana]
                  >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
```

```
Seq. No.      233625
Seq. ID      LIB3272-018-P1-K1-C5
Method       BLASTX
NCBI GI      g1361983
BLAST score   405
E value      1.0e-39
Match length  124
% identity    62
NCBI Description  ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_
                (Z49776) ARP protein [Arabidopsis thaliana]
```

```
Seq. No.      233626
Seq. ID       LIB3272-018-P1-K1-C6
Method        BLASTX
NCBI GI       g100525
BLAST score   599
E value       3.0e-62
Match length  123
% identity    25
NCBI Description  ubiquitin precursor UbB2 - common sunflower (fragment)
                  >gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein
                  [Helianthus annuus]
```

```
Seq. No.      233627
Seq. ID      LIB3272-018-P1-K1-C9
Method       BLASTX
NCBI GI      g119640
BLAST score   165
E value      2.0e-11
Match length  96
% identity    40
NCBI Description  1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
E8) >gi_82109_pir_S01642 ripening protein E8 - tomato
>gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon
esculentum]
```


09634016-104000

NCBI Description (AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana]
 Seq. No. 233639
 Seq. ID LIB3272-018-P1-K1-E12
 Method BLASTX
 NCBI GI g3892056
 BLAST score 274
 E value 2.0e-24
 Match length 72
 % identity 76
 NCBI Description (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No. 233640
 Seq. ID LIB3272-018-P1-K1-E2
 Method BLASTX
 NCBI GI g1839188
 BLAST score 459
 E value 7.0e-46
 Match length 102
 % identity 84
 NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 233641
 Seq. ID LIB3272-018-P1-K1-E3
 Method BLASTX
 NCBI GI g4539545
 BLAST score 685
 E value 2.0e-72
 Match length 135
 % identity 98
 NCBI Description (Y16644) PRCI [Nicotiana tabacum]

Seq. No. 233642
 Seq. ID LIB3272-018-P1-K1-E4
 Method BLASTX
 NCBI GI g1699024
 BLAST score 410
 E value 3.0e-40
 Match length 116
 % identity 66
 NCBI Description (U78866) gene1000 [Arabidopsis thaliana] >gi_1699057
 (U78870) unknown [Arabidopsis thaliana]

Seq. No. 233643
 Seq. ID LIB3272-018-P1-K1-E8
 Method BLASTX
 NCBI GI g3885328
 BLAST score 208
 E value 2.0e-16
 Match length 126
 % identity 33
 NCBI Description (AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 233644
 Seq. ID LIB3272-018-P1-K1-E9

Method	BLASTX
NCBI GI	g2462758
BLAST score	377
E value	3.0e-36
Match length	126
% identity	60
NCBI Description	(AC002292) putative RNA-binding protein [Arabidopsis thaliana]
Seq. No.	233645
Seq. ID	LIB3272-018-P1-K1-F11
Method	BLASTX
NCBI GI	g3482967
BLAST score	250
E value	8.0e-22
Match length	58
% identity	81
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	233646
Seq. ID	LIB3272-018-P1-K1-F2
Method	BLASTX
NCBI GI	g1351411
BLAST score	502
E value	6.0e-51
Match length	122
% identity	75
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B) >gi_1076553_pir_S49175 cysteine proteinase precursor - spring vetch >gi_2129906_pir_S68984 cysteine proteinase precursor - spring vetch >gi_510358_emb_CAA84383_ (Z34899) cysteine proteinase [Vicia sativa]
Seq. No.	233647
Seq. ID	LIB3272-018-P1-K1-F4
Method	BLASTX
NCBI GI	g2191150
BLAST score	166
E value	1.0e-11
Match length	67
% identity	63
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]
Seq. No.	233648
Seq. ID	LIB3272-018-P1-K1-G5
Method	BLASTX
NCBI GI	g2462748
BLAST score	591
E value	2.0e-61
Match length	122
% identity	93
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	233692
Seq. ID	LIB3272-019-P1-K1-G4
Method	BLASTX
NCBI GI	g1063415
BLAST score	371
E value	1.0e-35
Match length	106
% identity	70
NCBI Description	(L40948) K+ channel protein [Arabidopsis thaliana]
Seq. No.	233693
Seq. ID	LIB3272-019-P1-K1-G9
Method	BLASTX
NCBI GI	g1166450
BLAST score	257
E value	3.0e-22
Match length	56
% identity	82
NCBI Description	(X95262) Tfm5 [Lycopersicon esculentum]
Seq. No.	233694
Seq. ID	LIB3272-019-P1-K1-H1
Method	BLASTX
NCBI GI	g464846
BLAST score	404
E value	2.0e-39
Match length	79
% identity	94
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir_S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]
Seq. No.	233695
Seq. ID	LIB3272-019-P1-K1-H11
Method	BLASTX
NCBI GI	g3372233
BLAST score	414
E value	1.0e-40
Match length	102
% identity	75
NCBI Description	(AF019248) RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana]
Seq. No.	233696
Seq. ID	LIB3272-019-P1-K1-H12
Method	BLASTX
NCBI GI	g3023419
BLAST score	497
E value	2.0e-50
Match length	102
% identity	93
NCBI Description	CAFFEYOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEYOYL-COA 3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAMT) >gi_1934859_emb_CAA72911_ (Y12228) caffeoyl-CoA O-methyltransferase [Eucalyptus gunnii]

Seq. ID LIB3272-020-P1-K1-D9
 Method BLASTX
 NCBI GI g132944
 BLAST score 612
 E value 7.0e-64
 Match length 121
 % identity 92
 NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir_JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 233734
 Seq. ID LIB3272-020-P1-K1-E11
 Method BLASTX
 NCBI GI g3789799
 BLAST score 210
 E value 9.0e-17
 Match length 127
 % identity 9
 NCBI Description (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens] >gi_4557445_ref_NP_001259.1_pCHC1L RCC1-like G exchanging factor RLG

Seq. No. 233735
 Seq. ID LIB3272-020-P1-K1-E12
 Method BLASTX
 NCBI GI g2129987
 BLAST score 422
 E value 1.0e-41
 Match length 92
 % identity 85
 NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - potato (fragment) >gi_755187 (U17005) glyceraldehyde 3-phosphate dehydrogenase [Solanum tuberosum]

Seq. No. 233736
 Seq. ID LIB3272-020-P1-K1-E2
 Method BLASTX
 NCBI GI g4263706
 BLAST score 343
 E value 2.0e-32
 Match length 131
 % identity 55
 NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233737
 Seq. ID LIB3272-020-P1-K1-E5
 Method BLASTX
 NCBI GI g3789799
 BLAST score 210
 E value 9.0e-17
 Match length 127
 % identity 9
 NCBI Description (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens] >gi_4557445_ref_NP_001259.1_pCHC1L RCC1-like G exchanging factor RLG

Seq. ID LIB3272-020-P1-K1-H4
 Method BLASTX
 NCBI GI g4455364
 BLAST score 212
 E value 4.0e-17
 Match length 80
 % identity 51
 NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No. 233760
 Seq. ID LIB3272-020-P1-K1-H8
 Method BLASTX
 NCBI GI g584872
 BLAST score 318
 E value 2.0e-29
 Match length 114
 % identity 49
 NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_629475_pir_S39509 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - Norway spruce >gi_393443_emb_CAA51226_ (X72675) cinnamyl-alcohol dehydrogenase [Picea abies] >gi_3451286_emb_CAA05096_ (AJ001925) cinnamyl alcohol dehydrogenase [Picea abies] >gi_3451288_emb_CAA05097_ (AJ001926) cinnamyl alcohol dehydrogenase [Picea abies]

Seq. No. 233761
 Seq. ID LIB3272-021-P1-K1-A10
 Method BLASTX
 NCBI GI g2511574
 BLAST score 532
 E value 2.0e-54
 Match length 118
 % identity 93
 NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No. 233762
 Seq. ID LIB3272-021-P1-K1-A11
 Method BLASTX
 NCBI GI g2827559
 BLAST score 156
 E value 2.0e-10
 Match length 42
 % identity 69
 NCBI Description (AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 233763
 Seq. ID LIB3272-021-P1-K1-A12
 Method BLASTX
 NCBI GI g4456760
 BLAST score 482
 E value 1.0e-48
 Match length 110

Method BLASTX
 NCBI GI g2088654
 BLAST score 444
 E value 4.0e-44
 Match length 102
 % identity 84
 NCBI Description (AF002109) 60S acidic ribosomal protein P0 isolog
 [Arabidopsis thaliana]

Seq. No. 233769
 Seq. ID LIB3272-021-P1-K1-B12
 Method BLASTX
 NCBI GI g3643609
 BLAST score 425
 E value 6.0e-42
 Match length 133
 % identity 67
 NCBI Description (AC005395) putative Cys3His zinc finger protein
 [Arabidopsis thaliana]

Seq. No. 233770
 Seq. ID LIB3272-021-P1-K1-B2
 Method BLASTX
 NCBI GI g3342913
 BLAST score 158
 E value 1.0e-10
 Match length 128
 % identity 31
 NCBI Description (AF078916) oligopeptidase B [Trypanosoma brucei brucei]

Seq. No. 233771
 Seq. ID LIB3272-021-P1-K1-B3
 Method BLASTX
 NCBI GI g3913295
 BLAST score 340
 E value 3.0e-32
 Match length 77
 % identity 88
 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
 (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
 3-O-METHYLTRANSFERASE) (COMT) >gi_602588_emb_CAA58218_
 (X83217) caffeic O-methyltransferase [Prunus dulcis]

Seq. No. 233772
 Seq. ID LIB3272-021-P1-K1-B7
 Method BLASTX
 NCBI GI g4426565
 BLAST score 165
 E value 2.0e-11
 Match length 87
 % identity 40
 NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 233773
 Seq. ID LIB3272-021-P1-K1-B8
 Method BLASTX
 NCBI GI g2687584


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BLAST score      493
E value         6.0e-50
Match length    135
% identity      75
NCBI Description (AF033100) S-adenosylmethionine decarboxylase [Nicotiana
tabacum]
```

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Seq. No.      233774
Seq. ID      LIB3272-021-P1-K1-C1
Method       BLASTX
NCBI GI      g121953
BLAST score   189
E value      3.0e-14
Match length  43
% identity    88
NCBI Description HISTONE H1 >gi_81905_pir_S00033 histone H1.b - garden pea
               >gi_20762_emb_CAA29123_(X05636) H1 histone (AA 1-263)
               [Pisum sativum]
```

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Seq. No.          233775
Seq. ID           LIB3272-021-P1-K1-C12
Method            BLASTX
NCBI GI           g1706547
BLAST score       395
E value           8.0e-40
Match length      127
% identity        66
NCBI Description  GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM
                  PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE)
                  ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE)
                  >gi_2129912_pir_S65077 beta-1,3-glucanase class I
                  precursor - Para rubber tree >gi_1184668 (U22147)
                  beta-1,3-glucanase [Hevea brasiliensis]

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Seq. No.      233776
Seq. ID      LIB3272-021-P1-K1-C3
Method       BLASTX
NCBI GI      g3868758
BLAST score   410
E value      3.0e-40
Match length  77
% identity    94
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
```

```
Seq. No.      233777
Seq. ID       LIB3272-021-P1-K1-C5
Method        BLASTX
NCBI GI       g3694872
BLAST score   429
E value       2.0e-42
Match length  108
% identity    75
NCBI Description (AF092547) profilin [Ricinus communis]
```

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Seq. No.      233778
Seq. ID      LIB3272-021-P1-K1-C6
Method      BLASTX
```


NCBI GI g2160166
 BLAST score 483
 E value 1.0e-48
 Match length 133
 % identity 66
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233779
 Seq. ID LIB3272-021-P1-K1-C8
 Method BLASTX
 NCBI GI g3242721
 BLAST score 372
 E value 1.0e-35
 Match length 111
 % identity 60
 NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No. 233780
 Seq. ID LIB3272-021-P1-K1-D1
 Method BLASTX
 NCBI GI g2078350
 BLAST score 600
 E value 2.0e-62
 Match length 134
 % identity 87
 NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 233781
 Seq. ID LIB3272-021-P1-K1-D10
 Method BLASTX
 NCBI GI g3043432
 BLAST score 186
 E value 6.0e-14
 Match length 34
 % identity 100
 NCBI Description (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]

Seq. No. 233782
 Seq. ID LIB3272-021-P1-K1-D11
 Method BLASTX
 NCBI GI g543905
 BLAST score 446
 E value 2.0e-44
 Match length 106
 % identity 82
 NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
 brassinosteroid-regulated protein [Glycine max]

Seq. No. 233783
 Seq. ID LIB3272-021-P1-K1-D3
 Method BLASTX
 NCBI GI g2500354
 BLAST score 648
 E value 3.0e-69
 Match length 134
 % identity 91

Seq. No. 233789
 Seq. ID LIB3272-021-P1-K1-E5
 Method BLASTX
 NCBI GI g3776559
 BLAST score 325
 E value 3.0e-30
 Match length 95
 % identity 64
 NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No. 233790
 Seq. ID LIB3272-021-P1-K1-E7
 Method BLASTX
 NCBI GI g3600058
 BLAST score 328
 E value 1.0e-30
 Match length 90
 % identity 79
 NCBI Description (AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No. 233791
 Seq. ID LIB3272-021-P1-K1-E8
 Method BLASTX
 NCBI GI g3876865
 BLAST score 158
 E value 1.0e-10
 Match length 122
 % identity 36
 NCBI Description (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No. 233792
 Seq. ID LIB3272-021-P1-K1-F10
 Method BLASTX
 NCBI GI g3702332
 BLAST score 390
 E value 7.0e-38
 Match length 108
 % identity 68
 NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 233793
 Seq. ID LIB3272-021-P1-K1-F11
 Method BLASTX
 NCBI GI g4454043
 BLAST score 338
 E value 7.0e-32
 Match length 112
 % identity 57
 NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Method BLASTX
 NCBI GI g1850546
 BLAST score 403
 E value 2.0e-39
 Match length 103
 % identity 79
 NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No. 233800
 Seq. ID LIB3272-021-P1-K1-G10
 Method BLASTX
 NCBI GI g3337366
 BLAST score 203
 E value 5.0e-16
 Match length 106
 % identity 23
 NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]

Seq. No. 233801
 Seq. ID LIB3272-021-P1-K1-G11
 Method BLASTX
 NCBI GI g3175990
 BLAST score 350
 E value 3.0e-33
 Match length 72
 % identity 92
 NCBI Description (AJ005836) GDP dissociation inhibitor [Cicer arietinum]

Seq. No. 233802
 Seq. ID LIB3272-021-P1-K1-G12
 Method BLASTX
 NCBI GI g419789
 BLAST score 296
 E value 8.0e-27
 Match length 86
 % identity 67
 NCBI Description hypothetical protein - potato

Seq. No. 233803
 Seq. ID LIB3272-021-P1-K1-G2
 Method BLASTX
 NCBI GI g543867
 BLAST score 112
 E value 1.0e-11
 Match length 95
 % identity 56
 NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
 >gi_1076684_pir_A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato
 >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gamma subunit [Ipomoea batatas]

Seq. No. 233804
 Seq. ID LIB3272-021-P1-K1-G3
 Method BLASTX
 NCBI GI g117549

Match length 116
 % identity 73
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 233810
 Seq. ID LIB3272-021-P1-K1-H3
 Method BLASTX
 NCBI GI g267082
 BLAST score 559
 E value 1.0e-57
 Match length 106
 % identity 94
 NCBI Description TUBULIN BETA-8 CHAIN >gi_320189_pir_JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No. 233811
 Seq. ID LIB3272-021-P1-K1-H4
 Method BLASTX
 NCBI GI g100203
 BLAST score 311
 E value 1.0e-28
 Match length 107
 % identity 60
 NCBI Description cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No. 233812
 Seq. ID LIB3272-021-P1-K1-H5
 Method BLASTX
 NCBI GI g3643609
 BLAST score 428
 E value 3.0e-42
 Match length 135
 % identity 66
 NCBI Description (AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No. 233813
 Seq. ID LIB3272-021-P1-K1-H6
 Method BLASTX
 NCBI GI g1279588
 BLAST score 411
 E value 3.0e-40
 Match length 117
 % identity 68
 NCBI Description (Z71749) glutathione S-transferase [Nicotiana glumbaginifolia]

Seq. No. 233814
 Seq. ID LIB3272-021-P1-K1-H7
 Method BLASTX
 NCBI GI g1702983
 BLAST score 351
 E value 3.0e-33
 Match length 110


```
>gi_81837_pir_S22523 asparaginase (EC 3.5.1.1) - tree
lupine (fragment) >gi_19137_emb_CAA36824_ (X52588)
asparaginase [Lupinus arboreus]
```

```
Seq. No.          233820
Seq. ID           LIB3272-022-P1-K1-A6
Method            BLASTX
NCBI GI           g3334147
BLAST score       509
E value           9.0e-52
Match length      138
% identity        74
NCBI Description   ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I
                   chitinase [Gossypium hirsutum]
```

```
Seq. No.      233821
Seq. ID       LIB3272-022-P1-K1-B1
Method        BLASTX
NCBI GI       g445613
BLAST score   386
E value       2.0e-37
Match length  120
% identity    66
NCBI Description ribosomal protein L7 [Solanum tuberosum]
```

```
Seq. No.          233822
Seq. ID           LIB3272-022-P1-K1-B2
Method            BLASTX
NCBI GI           g3694872
BLAST score       502
E value           5.0e-51
Match length      118
% identity         80
NCBI Description   (AF092547) profilin [Ricinus communis]
```

```
Seq. No.      233823
Seq. ID       LIB3272-022-P1-K1-B5
Method        BLASTX
NCBI GI       g1657948
BLAST score   412
E value       2.0e-40
Match length  106
% identity    79
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
```

```
Seq. No.      233824
Seq. ID ..    LIB3272-022-P1-K1-B8
Method        BLASTX
NCBI GI       g3860255
BLAST score    294
E value        1.0e-26
Match length   143
% identity     46
NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	233825
Seq. ID	LIB3272-022-P1-K1-B9

[illegible]

```
Seq. No.      233830
Seq. ID      LIB3272-022-P1-K1-C5
Method       BLASTX
NCBI GI      g542200
BLAST score   452
E value      4.0e-45
Match length  125
% identity    66
NCBI Description  hypothetical protein - garden asparagus
                  >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus
                  officinalis]
```

```
Seq. No.          233831
Seq. ID           LIB3272-022-P1-K1-C8
Method            BLASTX
NCBI GI           g1946355
BLAST score       171
E value           4.0e-12
Match length      58
% identity        53
NCBI Description   [U93215) maize transposon MuDR mudrA protein isolog
                  [Arabidopsis thaliana] >gi_2880040 (AC002340) maize
                  transposon MuDR mudrA-like protein [Arabidopsis thaliana]
```

```
Seq. No.      233832
Seq. ID       LIB3272-022-P1-K1-C9
Method        BLASTX
NCBI GI       g445613
BLAST score    423
E value       1.0e-41
Match length   128
% identity     67
NCBI Description  ribosomal protein L7 [Solanum tuberosum]
```

```
Seq. No.      233833
Seq. ID      LIB3272-022-P1-K1-D11
Method       BLASTX
NCBI GI      g2499945
BLAST score   355
```


E value 9.0e-34
 Match length 112
 % identity 62
 NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir_S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No. 233834
 Seq. ID LIB3272-022-P1-K1-D2
 Method BLASTX
 NCBI GI g1703375
 BLAST score 490
 E value 1.0e-49
 Match length 95
 % identity 100
 NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No. 233835
 Seq. ID LIB3272-022-P1-K1-D3
 Method BLASTX
 NCBI GI g3386621
 BLAST score 592
 E value 2.0e-61
 Match length 126
 % identity 92
 NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 233836
 Seq. ID LIB3272-022-P1-K1-D4
 Method BLASTX
 NCBI GI g3738324
 BLAST score 260
 E value 1.0e-22
 Match length 82
 % identity 55
 NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No. 233837
 Seq. ID LIB3272-022-P1-K1-D5
 Method BLASTX
 NCBI GI g1928981
 BLAST score 474
 E value 1.0e-47
 Match length 114
 % identity 77
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 233838
 Seq. ID LIB3272-022-P1-K1-D6
 Method BLASTX
 NCBI GI g112863

BLAST score	256
E value	4.0e-22
Match length	74
% identity	64
NCBI Description	STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR >gi_100227_pir_S12209 hypothetical protein - tomato >gi_19162_emb_CAA38979_ (X55193) 9612 [Lycopersicon esculentum]
Seq. No.	233839
Seq. ID	LIB3272-022-P1-K1-D8
Method	BLASTX
NCBI GI	g475048
BLAST score	624
E value	3.0e-65
Match length	133
% identity	64
NCBI Description	(X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana]
Seq. No.	233840
Seq. ID	LIB3272-022-P1-K1-E11
Method	BLASTX
NCBI GI	g3551247
BLAST score	486
E value	4.0e-49
Match length	144
% identity	68
NCBI Description	(AB012703) 181 [Daucus carota]
Seq. No.	233841
Seq. ID	LIB3272-022-P1-K1-E12
Method	BLASTX
NCBI GI	g3329368
BLAST score	129
E value	3.0e-11
Match length	100
% identity	42
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]
Seq. No.	233842
Seq. ID	LIB3272-022-P1-K1-E3
Method	BLASTX
NCBI GI	g2791834
BLAST score	333
E value	7.0e-35
Match length	127
% identity	67
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.	233843
Seq. ID	LIB3272-022-P1-K1-E4
Method	BLASTX
NCBI GI	g999542
BLAST score	354
E value	1.0e-33
Match length	104

% identity	64
NCBI Description	Spinacia oleracea >gi_999543_pdb_1GYL_B Spinacia oleracea
Seq. No.	233844
Seq. ID	LIB3272-022-P1-K1-E5
Method	BLASTX
NCBI GI	g417719
BLAST score	620
E value	9.0e-65
Match length	140
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_2144763_pir_R3HUS3 ribosomal protein S3 - human >gi_233042_bbs_42659 (S42658) S3 ribosomal protein [human, colon, Peptide, 243 aa] [Homo sapiens] >gi_555941 (U14990) ribosomal protein S3 [Homo sapiens] >gi_555943 (U14991) ribosomal protein S3 [Homo sapiens] >gi_555945 (U14992) ribosomal protein S3 [Homo sapiens]
Seq. No.	233845
Seq. ID	LIB3272-022-P1-K1-E7
Method	BLASTX
NCBI GI	g549063
BLAST score	636
E value	1.0e-66
Match length	144
% identity	83
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]
Seq. No.	233846
Seq. ID	LIB3272-022-P1-K1-E8
Method	BLASTX
NCBI GI	g3608139
BLAST score	353
E value	9.0e-38
Match length	141
% identity	64
NCBI Description	(AC005314) putative fibrillin [Arabidopsis thaliana]
Seq. No.	233847
Seq. ID	LIB3272-022-P1-K1-F1
Method	BLASTX
NCBI GI	g441457
BLAST score	562
E value	5.0e-58
Match length	109
% identity	97
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]
Seq. No.	233848
Seq. ID	LIB3272-022-P1-K1-F10
Method	BLASTX
NCBI GI	g629483

BLAST score 301
 E value 2.0e-27
 Match length 125
 % identity 50
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula
 pendula]

Seq. No. 233849
 Seq. ID LIB3272-022-P1-K1-F11
 Method BLASTX
 NCBI GI g2911044
 BLAST score 369
 E value 2.0e-35
 Match length 118
 % identity 60
 NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 233850
 Seq. ID LIB3272-022-P1-K1-F2
 Method BLASTX
 NCBI GI g1766046
 BLAST score 341
 E value 3.0e-32
 Match length 72
 % identity 86
 NCBI Description (U81993) NAD+ dependent isocitrate dehydrogenase subunit 1
 [Arabidopsis thaliana]

Seq. No. 233851
 Seq. ID LIB3272-022-P1-K1-F3
 Method BLASTX
 NCBI GI g1638842
 BLAST score 390
 E value 7.0e-38
 Match length 93
 % identity 78
 NCBI Description (Z49697) cysteine proteinase inhibitor [Ricinus communis]

Seq. No. 233852
 Seq. ID LIB3272-022-P1-K1-F4
 Method BLASTX
 NCBI GI g629858
 BLAST score 545
 E value 5.0e-56
 Match length 126
 % identity 82
 NCBI Description protein kinase C inhibitor - maize

Seq. No. 233853
 Seq. ID LIB3272-022-P1-K1-F5
 Method BLASTX
 NCBI GI g3980393
 BLAST score 384
 E value 4.0e-37
 Match length 110

09684046-101000

% identity 63
NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 233854
Seq. ID LIB3272-022-P1-K1-F6
Method BLASTX
NCBI GI g3980393
BLAST score 210
E value 6.0e-27
Match length 110
% identity 53
NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 233855
Seq. ID LIB3272-022-P1-K1-F8
Method BLASTX
NCBI GI g3885515
BLAST score 443
E value 5.0e-44
Match length 101
% identity 81
NCBI Description (AF084202) similar to ribosomal protein S26 [Medicago sativa]

Seq. No. 233856
Seq. ID LIB3272-022-P1-K1-G1
Method BLASTX
NCBI GI g3759184
BLAST score 235
E value 1.0e-19
Match length 82
% identity 60
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 233857
Seq. ID LIB3272-022-P1-K1-G10
Method BLASTX
NCBI GI g1931639
BLAST score 237
E value 5.0e-20
Match length 97
% identity 44
NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No. 233858
Seq. ID LIB3272-022-P1-K1-G5
Method BLASTX
NCBI GI g4406816
BLAST score 624
E value 3.0e-65
Match length 123
% identity 93
NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 233859

[*Arabidopsis thaliana*]

```
Seq. No.      233885
Seq. ID       LIB3272-023-P1-K1-C8
Method        BLASTX
NCBI GI       g1619300
BLAST score    315
E value       5.0e-29
Match length   79
% identity     73
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
```

```
Seq. No.      233886
Seq. ID      LIB3272-023-P1-K1-C9
Method       BLASTX
NCBI GI      g1709498
BLAST score   506
E value      2.0e-51
Match length 135
% identity   70
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
                thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                [Arabidopsis thaliana]
```

```
Seq. No.          233887
Seq. ID          LIB3272-023-P1-K1-D2
Method           BLASTX
NCBI GI          g2865623
BLAST score      300
E value          2.0e-41
Match length     129
% identity       71
NCBI Description (AF045286)
                  GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                  [Arabidopsis thaliana]
```

```
Seq. No.      233888
Seq. ID       LIB3272-023-P1-K1-D3
Method        BLASTX
NCBI GI       g1717953
BLAST score    216
E value       2.0e-17
Match length  114
% identity    46
NCBI Description  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 5
                PRECURSOR, (RIESKE IRON-SULFUR PROTEIN 5) (RISP5) >gi_530055
                (L16813) Rieske iron-sulfur protein [Nicotiana tabacum]
```

```
Seq. No.          233889
Seq. ID           LIB3272-023-P1-K1-D5
Method            BLASTX
NCBI GI           gl234900
BLAST score       169
E value           7.0e-12
Match length      116
% identity        41
```


NCBI Description (X92489) homeobox-leucine zipper protein [Glycine max]

Seq. No. 233890
 Seq. ID LIB3272-023-P1-K1-D7
 Method BLASTX
 NCBI GI g3914430
 BLAST score 743
 E value 3.0e-79
 Match length 145
 % identity 98
 NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
 >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No. 233891
 Seq. ID LIB3272-023-P1-K1-D8
 Method BLASTX
 NCBI GI g3068809
 BLAST score 536
 E value 6.0e-55
 Match length 127
 % identity 83
 NCBI Description (AF059295) Skp1 homolog [Arabidopsis thaliana]

Seq. No. 233892
 Seq. ID LIB3272-023-P1-K1-D9
 Method BLASTX
 NCBI GI g3157951
 BLAST score 201
 E value 8.0e-17
 Match length 86
 % identity 67
 NCBI Description (AC002131) Contains similarity to vesicle trafficking protein gb_U91538 from Mus musculus. ESTs gb_F15494 and gb_F14097 come from this gene. [Arabidopsis thaliana]

Seq. No. 233893
 Seq. ID LIB3272-023-P1-K1-E12
 Method BLASTX
 NCBI GI g1172002
 BLAST score 591
 E value 2.0e-61
 Match length 143
 % identity 76
 NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_556424 (L36822)
 phenylalanine ammonia lyase [Stylosanthes humilis]

Seq. No. 233894
 Seq. ID LIB3272-023-P1-K1-E2
 Method BLASTX
 NCBI GI g2462931
 BLAST score 157
 E value 2.0e-10
 Match length 88
 % identity 50
 NCBI Description (Z83833) UDP-glucose:sterol glucosyltransferase


```
% identity      50
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
```

```
Seq. No.      233911
Seq. ID       LIB3272-023-P1-K1-G2
Method        BLASTX
NCBI GI       g1710530
BLAST score    666
E value        4.0e-70
Match length   134
% identity     89
NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir_S71256
                ribosomal protein L27a - Arabidopsis thaliana
                >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                L27a [Arabidopsis thaliana]
```

Seq. No.	233912
Seq. ID	LIB3272-023-P1-K1-G4
Method	BLASTX
NCBI GI	g2245108
BLAST score	197
E value	3.0e-15
Match length	45
% identity	87
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	233913
Seq. ID	LIB3272-023-P1-K1-G6
Method	BLASTX
NCBI GI	g4558659
BLAST score	603
E value	9.0e-63
Match length	145
% identity	73
NCBI Description	(AC007063) unknown protein [Arabidopsis thaliana]

```
Seq. No.          233915
Seq. ID           LIB3272-023-P1-K1-H11
Method            BLASTX
NCBI GI           g3695023
BLAST score       387
E value           2.0e-37
Match length      146
% identity         52
NCBI Description   (AF055850) unknown [Arabidopsis thaliana]
```


40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 233936
 Seq. ID LIB3272-024-P1-K1-B7
 Method BLASTX
 NCBI GI g629483
 BLAST score 331
 E value 7.0e-31
 Match length 125
 % identity 54
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula
 pendula]

Seq. No. 233937
 Seq. ID LIB3272-024-P1-K1-B8
 Method BLASTX
 NCBI GI g3158376
 BLAST score 488
 E value 2.0e-49
 Match length 131
 % identity 75
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233938
 Seq. ID LIB3272-024-P1-K1-C1
 Method BLASTX
 NCBI GI g2252836
 BLAST score 300
 E value 2.0e-27
 Match length 86
 % identity 67
 NCBI Description (AF013293) contains weak similarity to S. cerevisiae BOB1
 protein (PIR:S45444) [Arabidopsis thaliana]

Seq. No. 233939
 Seq. ID LIB3272-024-P1-K1-C2
 Method BLASTX
 NCBI GI g1730109
 BLAST score 475
 E value 7.0e-48
 Match length 112
 % identity 82
 NCBI Description LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
 HYDROXYLASE) >gi_499022_emb_CAA53580_ (X75966)
 leucoanthocyanidin dioxygenase [Vitis vinifera]

Seq. No. 233940
 Seq. ID LIB3272-024-P1-K1-C4
 Method BLASTX
 NCBI GI g3980393
 BLAST score 399
 E value 7.0e-39
 Match length 122
 % identity 61
 NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis

09067-1

Seq. No.	233945
Seq. ID	LIB3272-024-P1-K1-D5
Method	BLASTX
NCBI GI	g2529683
BLAST score	343
E value	2.0e-32
Match length	129
% identity	57
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]
Seq. No.	233946
Seq. ID	LIB3272-024-P1-K1-D6
Method	BLASTX
NCBI GI	g2791804
BLAST score	186
E value	6.0e-14
Match length	62
% identity	58
NCBI Description	(AF041432) bet3 [Homo sapiens] >gi_3413800_emb_CAA11902_ (AJ224335) hBET3 protein [Homo sapiens]
Seq. No.	233947
Seq. ID	LIB3272-024-P1-K1-D9
Method	BLASTX
NCBI GI	g1408471
BLAST score	468
E value	6.0e-47
Match length	106
% identity	79
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]
Seq. No.	233948
Seq. ID	LIB3272-024-P1-K1-E10
Method	BLASTX
NCBI GI	g464981
BLAST score	465
E value	1.0e-46
Match length	87
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.	233949
Seq. ID	LIB3272-024-P1-K1-E12
Method	BLASTX
NCBI GI	g2501578
BLAST score	502
E value	2.0e-55
Match length	124
% identity	97
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir_S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No. 233950
 Seq. ID LIB3272-024-P1-K1-E2
 Method BLASTX
 NCBI GI g3142294
 BLAST score 656
 E value 5.0e-69
 Match length 137
 % identity 91
 NCBI Description (AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from *S. pombe*. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [*Arabidopsis thaliana*]

Seq. No. 233951
 Seq. ID LIB3272-024-P1-K1-E4
 Method BLASTX
 NCBI GI g730241
 BLAST score 258
 E value 2.0e-22
 Match length 103
 % identity 51
 NCBI Description DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) >gi_473947_dbj_BAA06126_ (D29643) similar to *Canis* oligosaccharyltransferase 48 kDa subunit (M98392). [*Homo sapiens*]

Seq. No. 233952
 Seq. ID LIB3272-024-P1-K1-E5
 Method BLASTX
 NCBI GI g2286153
 BLAST score 507
 E value 1.0e-51
 Match length 105
 % identity 96
 NCBI Description (AF007581) cytoplasmic malate dehydrogenase [*Zea mays*]

Seq. No. 233953
 Seq. ID LIB3272-024-P1-K1-E6
 Method BLASTX
 NCBI GI g2499945
 BLAST score 167
 E value 7.0e-12
 Match length 79
 % identity 47
 NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir_S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - *Arabidopsis thaliana* >gi_443818_emb_CAA50686_ (X71842) pyrE-F [*Arabidopsis thaliana*]

Seq. No. 233954
 Seq. ID LIB3272-024-P1-K1-E7
 Method BLASTX

NCBI GI g3913413
 BLAST score 268
 E value 2.0e-23
 Match length 58
 % identity 90
 NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 1 (ADOMETDC 1) (SAMDC 1) (SAMDC9) >gi_1155240 (U38526)
 S-adenosylmethionine decarboxylase 1 [Dianthus caryophyllus] >gi_2406585 (U94786) S-adenosylmethionine decarboxylase [Dianthus caryophyllus]

Seq. No. 233955
 Seq. ID LIB3272-024-P1-K1-E8
 Method BLASTX
 NCBI GI g1168727
 BLAST score 386
 E value 2.0e-37
 Match length 105
 % identity 67
 NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_474300_dbj_BAA03099_ (D13991) cinnamyl alcohol dehydrogenase [Aralia cordata] >gi_745086_prf_2015401A cinnamoyl alcohol dehydrogenase [Aralia cordata]

Seq. No. 233956
 Seq. ID LIB3272-024-P1-K1-E9
 Method BLASTX
 NCBI GI g2129739
 BLAST score 302
 E value 1.0e-27
 Match length 70
 % identity 89
 NCBI Description shaggy-like kinase etha - Arabidopsis thaliana >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947) shaggy-like kinase etha [Arabidopsis thaliana]

Seq. No. 233957
 Seq. ID LIB3272-024-P1-K1-F10
 Method BLASTX
 NCBI GI g2760837
 BLAST score 199
 E value 2.0e-15
 Match length 89
 % identity 40
 NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 233958
 Seq. ID LIB3272-024-P1-K1-F11
 Method BLASTX
 NCBI GI g4314355
 BLAST score 323
 E value 6.0e-30
 Match length 97
 % identity 59
 NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	233964
Seq. ID	LIB3272-024-P1-K1-G2
Method	BLASTX
NCBI GI	g2253411
BLAST score	194
E value	8.0e-15
Match length	65
% identity	48
NCBI Description	(AF007219) PP2A inhibitor [Tetraodon fluviatilis]
Seq. No.	233965
Seq. ID	LIB3272-024-P1-K1-G3
Method	BLASTX
NCBI GI	g1922938
BLAST score	220
E value	8.0e-18
Match length	129
% identity	36
NCBI Description	(AC000106) Similar to Caenorhabditis hypothetical protein CO7A9.11 (gb_Z29094). [Arabidopsis thaliana]
Seq. No.	233966
Seq. ID	LIB3272-024-P1-K1-G5
Method	BLASTX
NCBI GI	g2267567
BLAST score	403
E value	2.0e-39
Match length	87
% identity	87
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]
Seq. No.	233967
Seq. ID	LIB3272-024-P1-K1-G6
Method	BLASTX
NCBI GI	g3023847
BLAST score	555
E value	4.0e-57
Match length	116
% identity	35
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]
Seq. No.	233968
Seq. ID	LIB3272-024-P1-K1-G7
Method	BLASTX
NCBI GI	g2129915
BLAST score	299
E value	4.0e-27
Match length	97
% identity	61
NCBI Description	ferredoxin precursor - sweet orange >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]

Seq. No.	233969
Seq. ID	LIB3272-024-P1-K1-G8
Method	BLASTX
NCBI GI	g1762933
BLAST score	458
E value	9.0e-46
Match length	116
% identity	78
NCBI Description	(U66263) tumor-related protein [Nicotiana tabacum]
Seq. No.	233970
Seq. ID	LIB3272-024-P1-K1-G9
Method	BLASTX
NCBI GI	g2832708
BLAST score	280
E value	6.0e-25
Match length	107
% identity	50
NCBI Description	(AL021713) beta-1, 3-glucanase-like protein [Arabidopsis thaliana]
Seq. No.	233971
Seq. ID	LIB3272-024-P1-K1-H10
Method	BLASTX
NCBI GI	g1706326
BLAST score	497
E value	2.0e-50
Match length	114
% identity	82
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_2146786_pir_S65470 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC1) - Garden pea >gi_1177603_emb_CAA91444_ (Z66543) pyruvate decarboxylase [Pisum sativum]
Seq. No.	233972
Seq. ID	LIB3272-024-P1-K1-H3
Method	BLASTX
NCBI GI	g267082
BLAST score	620
E value	9.0e-65
Match length	119
% identity	95
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir_JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]
Seq. No.	233973
Seq. ID	LIB3272-024-P1-K1-H4
Method	BLASTX
NCBI GI	g131385
BLAST score	542
E value	1.0e-55
Match length	134
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

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33792

E value 2.0e-20
 Match length 114
 % identity 47
 NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No. 233979
 Seq. ID LIB3272-026-P1-K1-A9
 Method BLASTX
 NCBI GI g2984709
 BLAST score 402
 E value 3.0e-39
 Match length 82
 % identity 91
 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 233980
 Seq. ID LIB3272-026-P1-K1-B1
 Method BLASTX
 NCBI GI g2984709
 BLAST score 468
 E value 6.0e-47
 Match length 97
 % identity 90
 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 233981
 Seq. ID LIB3272-026-P1-K1-B10
 Method BLASTX
 NCBI GI g1166450
 BLAST score 294
 E value 1.0e-26
 Match length 63
 % identity 83
 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]

Seq. No. 233982
 Seq. ID LIB3272-026-P1-K1-B12
 Method BLASTX
 NCBI GI g4481934
 BLAST score 163
 E value 3.0e-11
 Match length 105
 % identity 14
 NCBI Description (AL035640) CDA peptide synthetase I [Streptomyces coelicolor]

Seq. No. 233983
 Seq. ID LIB3272-026-P1-K1-B3
 Method BLASTX
 NCBI GI g3319921
 BLAST score 242
 E value 2.0e-20
 Match length 94
 % identity 57
 NCBI Description (AJ223388) Hev b 3 [Hevea brasiliensis]

Seq. ID LIB3272-026-P1-K1-C5
Method BLASTX
NCBI GI g2146797
BLAST score 442
E value 5.0e-44
Match length 116
% identity 43
NCBI Description protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
>gi_1134968 (U41385) protein disulphide isomerase PDI
[Ricinus communis] >gi_1587210_prf_2206331A protein
disulfide isomerase [Ricinus communis]

Seq. No. 233990
Seq. ID LIB3272-026-P1-K1-D12
Method BLASTX
NCBI GI g4538967
BLAST score 302
E value 2.0e-27
Match length 80
% identity 72
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
thaliana]

Seq. No. 233991
Seq. ID LIB3272-026-P1-K1-D4
Method BLASTX
NCBI GI g3158474
BLAST score 581
E value 3.0e-60
Match length 122
% identity 92
NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 233992
Seq. ID LIB3272-026-P1-K1-D5
Method BLASTX
NCBI GI g119640
BLAST score 176
E value 6.0e-13
Match length 78
% identity 51
NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
E8) >gi_82109_pir_S01642 ripening protein E8 - tomato
>gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon
esculentum]

Seq. No. 233993
Seq. ID LIB3272-026-P1-K1-E1
Method BLASTX
NCBI GI g3309084
BLAST score 386
E value 2.0e-37
Match length 88
% identity 89
NCBI Description (AF076252) calcineurin B-like protein 2 [Arabidopsis
thaliana]

Seq. ID LIB3272-026-P1-K1-G7
 Method BLASTX
 NCBI GI g1710780
 BLAST score 397
 E value 6.0e-39
 Match length 98
 % identity 77
 NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No. 234005
 Seq. ID LIB3272-026-P1-K1-H1
 Method BLASTX
 NCBI GI g417148
 BLAST score 345
 E value 1.0e-32
 Match length 122
 % identity 55
 NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir_A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]

Seq. No. 234006
 Seq. ID LIB3272-026-P1-K1-H10
 Method BLASTX
 NCBI GI g3776577
 BLAST score 199
 E value 2.0e-15
 Match length 95
 % identity 42
 NCBI Description (AC005388) T22H22.24 [Arabidopsis thaliana]

Seq. No. 234007
 Seq. ID LIB3272-026-P1-K1-H11
 Method BLASTX
 NCBI GI g2347189
 BLAST score 341
 E value 4.0e-32
 Match length 84
 % identity 79
 NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana] >gi_3150399 (AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No. 234008
 Seq. ID LIB3272-026-P1-K1-H9
 Method BLASTX
 NCBI GI g267069
 BLAST score 336
 E value 9.0e-32
 Match length 70
 % identity 87
 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) alpha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 234009
 Seq. ID LIB3272-027-P1-K1-A10
 Method BLASTX
 NCBI GI g2648355
 BLAST score 148
 E value 2.0e-09
 Match length 138
 % identity 32
 NCBI Description (AE000955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus]

Seq. No. 234010
 Seq. ID LIB3272-027-P1-K1-A2
 Method BLASTX
 NCBI GI g1362055
 BLAST score 360
 E value 3.0e-34
 Match length 79
 % identity 90
 NCBI Description phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - alfalfa >gi_603221 (U18239) 6-phosphogluconate dehydrogenase [Medicago sativa subsp. sativa]

Seq. No. 234011
 Seq. ID LIB3272-027-P1-K1-A4
 Method BLASTX
 NCBI GI g132944
 BLAST score 653
 E value 1.0e-68
 Match length 128
 % identity 93
 NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir_JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 234012
 Seq. ID LIB3272-027-P1-K1-A5
 Method BLASTX
 NCBI GI g4371284
 BLAST score 678
 E value 1.0e-71
 Match length 142
 % identity 91
 NCBI Description (AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No. 234013
 Seq. ID LIB3272-027-P1-K1-A6
 Method BLASTX
 NCBI GI g547712
 BLAST score 695
 E value 1.0e-73
 Match length 143
 % identity 95
 NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir_S38358 translation initiation factor eIF-4A

- rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic
initiation factor 4A [Oryza sativa]

Seq. No. 234014
Seq. ID LIB3272-027-P1-K1-A7
Method BLASTX
NCBI GI g3868758
BLAST score 420
E value 2.0e-41
Match length 105
% identity 73
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 234015
Seq. ID LIB3272-027-P1-K1-B2
Method BLASTX
NCBI GI g1352681
BLAST score 217
E value 2.0e-17
Match length 117
% identity 48
NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir_S55457
phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
thaliana >gi_633028_dbj_BAA07287_ (D38109) protein
phosphatase 2C [Arabidopsis thaliana]

Seq. No. 234016
Seq. ID LIB3272-027-P1-K1-B4
Method BLASTX
NCBI GI g2129670
BLAST score 450
E value 8.0e-45
Match length 132
% identity 65
NCBI Description phosphoinositide-specific phospholipase C - Arabidopsis
thaliana >gi_857374_dbj_BAA09432_ (D50804) phosphoinositide
specific phospholipase C [Arabidopsis thaliana]

Seq. No. 234017
Seq. ID LIB3272-027-P1-K1-B8
Method BLASTX
NCBI GI g3413511
BLAST score 553
E value 6.0e-57
Match length 137
% identity 80
NCBI Description (AJ000265) glucose-6-phosphate isomerase [Spinacia
oleracea]

Seq. No. 234018
Seq. ID LIB3272-027-P1-K1-B9
Method BLASTX
NCBI GI g2274915
BLAST score 410
E value 4.0e-40
Match length 113
% identity 69

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NCBI Description (AJ000081) beta-1,3-glucanase [Citrus sinensis]

Seq. No. 234019
 Seq. ID LIB3272-027-P1-K1-C1
 Method BLASTX
 NCBI GI g122770
 BLAST score 442
 E value 5.0e-44
 Match length 112
 % identity 79

NCBI Description HEMOGLOBIN II >gi_99509_pir_S13378 hemoglobin II - swamp oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina glauca]

Seq. No. 234020
 Seq. ID LIB3272-027-P1-K1-C11
 Method BLASTX
 NCBI GI g267075
 BLAST score 751
 E value 4.0e-80
 Match length 144
 % identity 95

NCBI Description TUBULIN BETA-2 CHAIN >gi_388254_emb_CAA38614_ (X54845) beta-tubulin 2 [Pisum sativum]

Seq. No. 234021
 Seq. ID LIB3272-027-P1-K1-C2
 Method BLASTX
 NCBI GI g167367
 BLAST score 139
 E value 2.0e-19
 Match length 86
 % identity 69

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 234022
 Seq. ID LIB3272-027-P1-K1-C3
 Method BLASTX
 NCBI GI g3881978
 BLAST score 325
 E value 4.0e-30
 Match length 83
 % identity 46

NCBI Description (Y11348) annexin-like protein [Medicago sativa]

Seq. No. 234023
 Seq. ID LIB3272-027-P1-K1-C6
 Method BLASTX
 NCBI GI g2388575
 BLAST score 239
 E value 4.0e-20
 Match length 133
 % identity 39

NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 234024
 Seq. ID LIB3272-027-P1-K1-D11

Method BLASTX
NCBI GI g120669
BLAST score 513
E value 3.0e-52
Match length 102
% identity 93
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 234025
Seq. ID LIB3272-027-P1-K1-D12
Method BLASTX
NCBI GI g120669
BLAST score 332
E value 5.0e-31
Match length 71
% identity 89
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 234026
Seq. ID LIB3272-027-P1-K1-D2
Method BLASTX
NCBI GI g2662343
BLAST score 594
E value 1.0e-61
Match length 113
% identity 100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 234027
Seq. ID LIB3272-027-P1-K1-D3
Method BLASTX
NCBI GI g3510540
BLAST score 365
E value 6.0e-35
Match length 85
% identity 74
NCBI Description (AF038815) expansin [Prunus armeniaca]

Seq. No. 234028
Seq. ID LIB3272-027-P1-K1-D4
Method BLASTX
NCBI GI g1168696
BLAST score 213
E value 5.0e-17
Match length 66
% identity 56
NCBI Description ALLERGEN BET V 3 (BET V III) >gi_629480_pir_S45011
allergen Bet v III - European white birch
>gi_1076247_pir_S46233 allergen - European white birch

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>gi_488605_emb_CAA55854_ (X79267) allergen [Betula pendula]

Seq. No. 234029
Seq. ID LIB3272-027-P1-K1-D6
Method BLASTX
NCBI GI g4210948
BLAST score 473
E value 2.0e-47
Match length 94
% identity 94
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 234030
Seq. ID LIB3272-027-P1-K1-D7
Method BLASTX
NCBI GI g3643602
BLAST score 263
E value 5.0e-23
Match length 103
% identity 54
NCBI Description (AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No. 234031
Seq. ID LIB3272-027-P1-K1-D8
Method BLASTX
NCBI GI g3023186
BLAST score 535
E value 8.0e-55
Match length 131
% identity 79
NCBI Description 14-3-3-LIKE PROTEIN 9 >gi_1771180_emb_CAA67373.1_ (X98865)
14-3-3 protein [Lycopersicon esculentum]

Seq. No. 234032
Seq. ID LIB3272-027-P1-K1-E1
Method BLASTX
NCBI GI g3023281
BLAST score 379
E value 2.0e-36
Match length 105
% identity 70
NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER
>gi_2065194_emb_CAA64475_ (X95098) ammonium transporter [Lycopersicon esculentum]

Seq. No. 234033
Seq. ID LIB3272-027-P1-K1-E10
Method BLASTX
NCBI GI g1279654
BLAST score 384
E value 4.0e-37
Match length 108
% identity 71
NCBI Description (X97351) peroxidase [Populus balsamifera subsp. trichocarpa]


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Seq. No.      234034
Seq. ID      LIB3272-027-P1-K1-E5
Method       BLASTX
NCBI GI      g2244806
BLAST score   277
E value      2.0e-24
Match length  88
% identity    59
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
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Seq. No.      234035
Seq. ID      LIB3272-027-P1-K1-E6
Method       BLASTX
NCBI GI      g1729971
BLAST score   270
E value      1.0e-23
Match length  69
% identity   70
NCBI Description  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein -
                rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                sativa]
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Seq. No.      234036
Seq. ID      LIB3272-027-P1-K1-E7
Method       BLASTX
NCBI GI      g3789911
BLAST score   156
E value      2.0e-10
Match length  87
% identity    40
NCBI Description (AF081802) developmental protein DG1118 [Dictyostelium
discoideum]
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Seq. No.      234037
Seq. ID      LIB3272-027-P1-K1-E8
Method       BLASTX
NCBI GI      g1707018
BLAST score   212
E value      2.0e-17
Match length  55
% identity    75
NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]
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Seq. No.          234038
Seq. ID           LIB3272-027-P1-K1-F1
Method            BLASTX
NCBI GI           g992706
BLAST score       543
E value           9.0e-56
Match length      105
% identity        91
NCBI Description   (U33758) UBC13 [Arabidopsis thaliana]
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Seq. No.      234039
Seq. ID      LIB3272-027-P1-K1-F10
Method      BLASTX
```


Match length	68
% identity	76
NCBI Description	(AJ009878) cysteine proteinase [Cicer arietinum]
Seq. No.	234045
Seq. ID	LIB3272-027-P1-K1-F8
Method	BLASTX
NCBI GI	g4150974
BLAST score	337
E value	9.0e-32
Match length	92
% identity	65
NCBI Description	(AJ224331) cystatin [Castanea sativa]
Seq. No.	234046
Seq. ID	LIB3272-027-P1-K1-F9
Method	BLASTX
NCBI GI	g2765837
BLAST score	156
E value	2.0e-10
Match length	41
% identity	71
NCBI Description	(Z96936) NAP16kDa protein [Arabidopsis thaliana]
Seq. No.	234047
Seq. ID	LIB3272-027-P1-K1-G1
Method	BLASTX
NCBI GI	g3184098
BLAST score	166
E value	1.0e-11
Match length	122
% identity	34
NCBI Description	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]
Seq. No.	234048
Seq. ID	LIB3272-027-P1-K1-G10
Method	BLASTX
NCBI GI	g1703108
BLAST score	702
E value	2.0e-74
Match length	144
% identity	98
NCBI Description	ACTIN 2/7 >gi_2129525_pir_S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir_S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]
Seq. No.	234049
Seq. ID	LIB3272-027-P1-K1-G11
Method	BLASTX
NCBI GI	g122007
BLAST score	338
E value	1.0e-31
Match length	98
% identity	70


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NCBI GI             g4104242
BLAST score         632
E value             3.0e-66
Match length        137
% identity           87
NCBI Description     (AF034266) palmitoyl-acyl carrier protein thioesterase
                    [Gossypium hirsutum]

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Seq. No.          234086
Seq. ID           LIB3272-028-P1-K1-D3
Method            BLASTX
NCBI GI           g2129726
BLAST score       560
E value           9.0e-58
Match length      120
% identity        87
NCBI Description  RNA polymerase II third largest chain RPB35.5A -
                  Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II
                  third largest subunit [Arabidopsis thaliana]
                  >gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA
                  polymerase II, third largest subunit [Arabidopsis thaliana]
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```
Seq. No.      234087
Seq. ID      LIB3272-028-P1-K1-D5
Method       BLASTX
NCBI GI      g4261517
BLAST score   361
E value      2.0e-34
Match length  85
% identity    78
NCBI Description (AF117334) cysteine proteinase inhibitor [Ipomoea batatas]
```

```
Seq. No.      234088
Seq. ID      LIB3272-028-P1-K1-D7
Method       BLASTX
NCBI GI      g2129915
BLAST score   507
E value      1.0e-51
Match length  131
% identity    72
NCBI Description  ferredoxin precursor - sweet orange
                  >gi_1360725_emb_CAA87068_(Z46944) non-photosynthetic
                  ferredoxin [Citrus sinensis]
```

```
Seq. No.      234089
Seq. ID       LIB3272-028-P1-K1-D8
Method        BLASTX
NCBI GI       g1850546
BLAST score    407
E value       8.0e-40
Match length   104
% identity     79
NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]
```

Seq. No.	234090
Seq. ID	LIB3272-028-P1-K1-D9


```

BLAST score      515
E value          2.0e-52
Match length     112
% identity       83
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
>gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
[Arabidopsis thaliana]

```

```
Seq. No.      234096
Seq. ID       LIB3272-028-P1-K1-E7
Method        BLASTX
NCBI GI       g167367
BLAST score   464
E value       1.0e-46
Match length  120
% identity    76
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
```

```
Seq. No.      234097
Seq. ID      LIB3272-028-P1-K1-E9
Method       BLASTX
NCBI GI      g3915031
BLAST score   700
E value      3.0e-74
Match length  132
% identity    99
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_
                (X95988) delta 9 stearyl-[acyl-carrier protein] desaturase
                [Gossypium hirsutum]
```

```
Seq. No.      234098
Seq. ID      LIB3272-028-P1-K1-F1
Method       BLASTX
NCBI GI      g2129579
BLAST score   748
E value      8.0e-80
Match length  136
% identity    94
NCBI Description Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
              Dwarf1 [Arabidopsis thaliana]
```

```
Seq. No.          234099
Seq. ID           LIB3272-028-P1-K1-F4
Method            BLASTX
NCBI GI           g20186
BLAST score       491
E value           1.0e-49
Match length      96
% identity        55
NCBI Description   (X65016) calmodulin [Oryza sativa]
                  >gi_3336950_emb_CAA74307_(Y13974) calmodulin [Zea mays]
                  >gi_4103961_(AF030034) calmodulin [Phaseolus vulgaris]
```

Seq. No. 234100
Seq. ID LIB3272-028-P1-K1-F5

Method BLASTX
 NCBI GI g464986
 BLAST score 522
 E value 3.0e-53
 Match length 96
 % identity 99
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_(Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_(X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1_(AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 234101
 Seq. ID LIB3272-028-P1-K1-F6
 Method BLASTX
 NCBI GI g2924521
 BLAST score 183
 E value 1.0e-13
 Match length 109
 % identity 43
 NCBI Description (AL022023) putative protein [Arabidopsis thaliana]

Seq. No. 234102
 Seq. ID LIB3272-028-P1-K1-F7
 Method BLASTX
 NCBI GI g585241
 BLAST score 193
 E value 1.0e-14
 Match length 98
 % identity 45
 NCBI Description HISTONE H1 >gi_629668_pir_S45662 histone H1 - tomato
 >gi_424100 (U03391) histone H1 [Lycopersicon esculentum]

Seq. No. 234103
 Seq. ID LIB3272-028-P1-K1-F9
 Method BLASTX
 NCBI GI g1841870
 BLAST score 344
 E value 2.0e-32
 Match length 93
 % identity 75
 NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No. 234104
 Seq. ID LIB3272-028-P1-K1-G11
 Method BLASTX
 NCBI GI g2829896
 BLAST score 395
 E value 2.0e-38
 Match length 133
 % identity 56

E value 6.0e-64
 Match length 142
 % identity 84
 NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No. 234126
 Seq. ID LIB3272-029-P1-K1-C8
 Method BLASTX
 NCBI GI g3608136
 BLAST score 231
 E value 2.0e-35
 Match length 89
 % identity 90
 NCBI Description (AC005314) defender against cell death [Arabidopsis thaliana]

Seq. No. 234127
 Seq. ID LIB3272-029-P1-K1-D10
 Method BLASTX
 NCBI GI g3377813
 BLAST score 190
 E value 2.0e-14
 Match length 61
 % identity 57
 NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]

Seq. No. 234128
 Seq. ID LIB3272-029-P1-K1-D2
 Method BLASTX
 NCBI GI g3158376
 BLAST score 151
 E value 5.0e-16
 Match length 121
 % identity 50
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 234129
 Seq. ID LIB3272-029-P1-K1-D3
 Method BLASTX
 NCBI GI g4467153
 BLAST score 483
 E value 1.0e-48
 Match length 104
 % identity 82
 NCBI Description (AL035540) putative thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 234130
 Seq. ID LIB3272-029-P1-K1-D4
 Method BLASTX
 NCBI GI g2501555
 BLAST score 315
 E value 5.0e-29
 Match length 114
 % identity 54
 NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148)

BLAST score 427
 E value 3.0e-42
 Match length 91
 % identity 88
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 234147
 Seq. ID LIB3272-029-P1-K1-F8
 Method BLASTX
 NCBI GI g1778376
 BLAST score 519
 E value 6.0e-53
 Match length 141
 % identity 68
 NCBI Description (U81288) PsRT17-1 [Pisum sativum]

Seq. No. 234148
 Seq. ID LIB3272-029-P1-K1-G1
 Method BLASTX
 NCBI GI g445612
 BLAST score 208
 E value 1.0e-16
 Match length 90
 % identity 52
 NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 234149
 Seq. ID LIB3272-029-P1-K1-G10
 Method BLASTX
 NCBI GI g2501449
 BLAST score 398
 E value 9.0e-39
 Match length 78
 % identity 97
 NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi_1668773_emb_CAA67922_ (X99608) ubiquitin-like protein [Oryza sativa]

Seq. No. 234150
 Seq. ID LIB3272-029-P1-K1-G12
 Method BLASTX
 NCBI GI g120669
 BLAST score 489
 E value 2.0e-49
 Match length 104
 % identity 89
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate

0969-0316

```
Seq. No.      234157
Seq. ID      LIB3272-029-P1-K1-H1
Method       BLASTX
NCBI GI      g4006881
BLAST score   277
E value      1.0e-24
Match length  115
% identity   55
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
```

Seq. No.	234158
Seq. ID	LIB3272-029-P1-K1-H10
Method	BLASTX
NCBI GI	g1263291
BLAST score	638
E value	7.0e-67
Match length	120
% identity	98
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

```
Seq. No.      234159
Seq. ID      LIB3272-029-P1-K1-H11
Method       BLASTX
NCBI GI      g1220196
BLAST score   550
E value      1.0e-56
Match length  120
% identity    88
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
```

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Seq. No.      234160
Seq. ID      LIB3272-029-P1-K1-H12
Method       BLASTX
NCBI GI      g3759184
BLAST score  254
```


E value 5.0e-22
 Match length 84
 % identity 62
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 234161
 Seq. ID LIB3272-029-P1-K1-H2
 Method BLASTX
 NCBI GI g167367
 BLAST score 640
 E value 4.0e-67
 Match length 138
 % identity 91
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 234162
 Seq. ID LIB3272-029-P1-K1-H4
 Method BLASTX
 NCBI GI g3600039
 BLAST score 283
 E value 8.0e-49
 Match length 140
 % identity 68
 NCBI Description (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No. 234163
 Seq. ID LIB3272-029-P1-K1-H7
 Method BLASTX
 NCBI GI g2921512
 BLAST score 455
 E value 2.0e-45
 Match length 112
 % identity 83
 NCBI Description (AF037460) GF14 protein [Fritillaria agrestis]

Seq. No. 234164
 Seq. ID LIB3272-030-P1-K1-A1
 Method BLASTX
 NCBI GI g1705812
 BLAST score 449
 E value 1.0e-44
 Match length 136
 % identity 62
 NCBI Description ACIDIC CHITINASE PRECURSOR >gi_1150686_emb_CAA92207_ (Z68123) acidic chitinase [Vitis vinifera]

Seq. No. 234165
 Seq. ID LIB3272-030-P1-K1-A10
 Method BLASTX
 NCBI GI g2347098
 BLAST score 512
 E value 4.0e-52
 Match length 107
 % identity 93
 NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific

Seq. ID LIB3272-030-P1-K1-B1
 Method BLASTX
 NCBI GI g3869088
 BLAST score 581
 E value 3.0e-60
 Match length 112
 % identity 98
 NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No. 234172
 Seq. ID LIB3272-030-P1-K1-B10
 Method BLASTX
 NCBI GI g118564
 BLAST score 466
 E value 7.0e-47
 Match length 104
 % identity 85
 NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir_DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber
 >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus]
 >gi_18275_emb_CAA32764_ (X14609) NADH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 234173
 Seq. ID LIB3272-030-P1-K1-B2
 Method BLASTX
 NCBI GI g2766452
 BLAST score 173
 E value 1.0e-12
 Match length 51
 % identity 63
 NCBI Description (AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]

Seq. No. 234174
 Seq. ID LIB3272-030-P1-K1-B5
 Method BLASTX
 NCBI GI g3559811
 BLAST score 168
 E value 7.0e-16
 Match length 88
 % identity 45
 NCBI Description (AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No. 234175
 Seq. ID LIB3272-030-P1-K1-B6
 Method BLASTX
 NCBI GI g1706326
 BLAST score 635
 E value 1.0e-66
 Match length 135
 % identity 87
 NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
 >gi_2146786_pir_S65470 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC1) - Garden pea >gi_1177603_emb_CAA91444_ (Z66543) pyruvate decarboxylase [Pisum sativum]

Method BLASTX
 NCBI GI g4521249
 BLAST score 433
 E value 6.0e-43
 Match length 114
 % identity 74
 NCBI Description (AB013912) DNA helicase [Mus musculus]

Seq. No. 234182
 Seq. ID LIB3272-030-P1-K1-C7
 Method BLASTX
 NCBI GI g1169009
 BLAST score 684
 E value 3.0e-72
 Match length 134
 % identity 90
 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
 (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
 3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir_S40146
 catechol O-methyltransferase (EC 2.1.1.6) - cider tree
 >gi_437777_emb_CAA52814_ (X74814) O-Methyltransferase
 [Eucalyptus gunnii]

Seq. No. 234183
 Seq. ID LIB3272-030-P1-K1-C8
 Method BLASTX
 NCBI GI g2244740
 BLAST score 167
 E value 9.0e-12
 Match length 44
 % identity 75
 NCBI Description (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No. 234184
 Seq. ID LIB3272-030-P1-K1-D10
 Method BLASTX
 NCBI GI g404670
 BLAST score 385
 E value 3.0e-37
 Match length 130
 % identity 59
 NCBI Description (L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934
 (AC003970) phytochrome A [Arabidopsis thaliana]

Seq. No. 234185
 Seq. ID LIB3272-030-P1-K1-D11
 Method BLASTX
 NCBI GI g3237190
 BLAST score 144
 E value 3.0e-09
 Match length 56
 % identity 54
 NCBI Description (AB014760) cystein proteinase inhibitor [Cucumis sativus]

Seq. No. 234186
 Seq. ID LIB3272-030-P1-K1-D12
 Method BLASTX

NCBI GI g2541876
 BLAST score 159
 E value 8.0e-11
 Match length 79
 % identity 49
 NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No. 234187
 Seq. ID LIB3272-030-P1-K1-D5
 Method BLASTX
 NCBI GI g4371284
 BLAST score 565
 E value 2.0e-58
 Match length 125
 % identity 86
 NCBI Description (AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No. 234188
 Seq. ID LIB3272-030-P1-K1-D8
 Method BLASTX
 NCBI GI g4115377
 BLAST score 270
 E value 9.0e-24
 Match length 85
 % identity 69
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 234189
 Seq. ID LIB3272-030-P1-K1-E12
 Method BLASTX
 NCBI GI g3763925
 BLAST score 332
 E value 4.0e-31
 Match length 70
 % identity 87
 NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]

Seq. No. 234190
 Seq. ID LIB3272-030-P1-K1-E2
 Method BLASTX
 NCBI GI g585973
 BLAST score 499
 E value 1.0e-50
 Match length 123
 % identity 83
 NCBI Description FRUCTOKINASE >gi_626018_pir_S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283 (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf_2108342A fructokinase [Solanum tuberosum]

Seq. No. 234191
 Seq. ID LIB3272-030-P1-K1-E3
 Method BLASTX
 NCBI GI g3128177
 BLAST score 486

% identity	22
NCBI Description	calmodulin [Chlamydomonas reinhardtii]
Seq. No.	234197
Seq. ID	LIB3272-030-P1-K1-F7
Method	BLASTX
NCBI GI	g3128228
BLAST score	626
E value	2.0e-65
Match length	128
% identity	91
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]
Seq. No.	234198
Seq. ID	LIB3272-030-P1-K1-F8
Method	BLASTX
NCBI GI	g167367
BLAST score	328
E value	1.0e-30
Match length	82
% identity	77
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]
Seq. No.	234199
Seq. ID	LIB3272-030-P1-K1-F9
Method	BLASTX
NCBI GI	g125887
BLAST score	194
E value	5.0e-15
Match length	102
% identity	46
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir_S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]
Seq. No.	234200
Seq. ID	LIB3272-030-P1-K1-G11
Method	BLASTX
NCBI GI	g217909
BLAST score	328
E value	1.0e-30
Match length	74
% identity	88
NCBI Description	(D14044) glycolate oxidase [Cucurbita sp.]
Seq. No.	234201
Seq. ID	LIB3272-030-P1-K1-G3
Method	BLASTX
NCBI GI	g3212854
BLAST score	272
E value	5.0e-24
Match length	126
% identity	59
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Method BLASTX
 NCBI GI g862931
 BLAST score 356
 E value 6.0e-34
 Match length 106
 % identity 69
 NCBI Description (U27179) acidic glucanase [Medicago sativa subsp. sativa]

Seq. No. 234208
 Seq. ID LIB3272-030-P1-K1-H10
 Method BLASTX
 NCBI GI g136057
 BLAST score 177
 E value 3.0e-13
 Match length 59
 % identity 61
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 >gi_99499_pir_A32187 (S)-tetrahydroberberine oxidase -
 Coptis japonica >gi_556171 (J04121) triosephosphate
 isomerase [Coptis japonica]

Seq. No. 234209
 Seq. ID LIB3272-030-P1-K1-H12
 Method BLASTX
 NCBI GI g2440044
 BLAST score 319
 E value 8.0e-30
 Match length 65
 % identity 91
 NCBI Description (AJ001293) major intrinsic protein PIPB [Craterostigma
 plantagineum]

Seq. No. 234210
 Seq. ID LIB3272-030-P1-K1-H2
 Method BLASTX
 NCBI GI g1928981
 BLAST score 537
 E value 4.0e-55
 Match length 114
 % identity 93
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
 oleracea var. botrytis]

Seq. No. 234211
 Seq. ID LIB3272-030-P1-K1-H3
 Method BLASTX
 NCBI GI g2829871
 BLAST score 129
 E value 4.0e-09
 Match length 93
 % identity 44
 NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 234212
 Seq. ID LIB3272-030-P1-K1-H9
 Method BLASTX
 NCBI GI g1107526

BLAST score 235
 E value 6.0e-20
 Match length 70
 % identity 61
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 234213
 Seq. ID LIB3272-031-P1-K1-A10
 Method BLASTX
 NCBI GI g1653767
 BLAST score 434
 E value 5.0e-43
 Match length 134
 % identity 59
 NCBI Description (D90916) oligopeptidase A [Synechocystis sp.]

Seq. No. 234214
 Seq. ID LIB3272-031-P1-K1-A3
 Method BLASTX
 NCBI GI g131385
 BLAST score 438
 E value 2.0e-43
 Match length 130
 % identity 70
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
 SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
 THYLAKOID MEMBRANE PROTEIN)

Seq. No. 234215
 Seq. ID LIB3272-031-P1-K1-A4
 Method BLASTX
 NCBI GI g548852
 BLAST score 361
 E value 2.0e-34
 Match length 82
 % identity 80
 NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal
 protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
 subunit ribosomal protein [Oryza sativa]

Seq. No. 234216
 Seq. ID LIB3272-031-P1-K1-A7
 Method BLASTX
 NCBI GI g1709498
 BLAST score 514
 E value 2.0e-52
 Match length 129
 % identity 74
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
 thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
 [Arabidopsis thaliana]

Seq. No. 234217
 Seq. ID LIB3272-031-P1-K1-B12
 Method BLASTX
 NCBI GI g3158376

NCBI GI g2738248
 BLAST score 508
 E value 1.0e-51
 Match length 138
 % identity 76
 NCBI Description (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No. 234228
 Seq. ID LIB3272-031-P1-K1-C6
 Method BLASTX
 NCBI GI g3980393
 BLAST score 262
 E value 6.0e-27
 Match length 102
 % identity 64
 NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 234229
 Seq. ID LIB3272-031-P1-K1-D1
 Method BLASTX
 NCBI GI g2388689
 BLAST score 217
 E value 2.0e-17
 Match length 84
 % identity 55
 NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 234230
 Seq. ID LIB3272-031-P1-K1-D12
 Method BLASTX
 NCBI GI g1657948
 BLAST score 385
 E value 2.0e-37
 Match length 104
 % identity 74
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 234231
 Seq. ID LIB3272-031-P1-K1-D2
 Method BLASTX
 NCBI GI g4049354
 BLAST score 689
 E value 7.0e-73
 Match length 137
 % identity 96
 NCBI Description (AL034567) glycine hydroxymethyltransferase (EC 2.1.2.1)-like protein [Arabidopsis thaliana]

Seq. No. 234232
 Seq. ID LIB3272-031-P1-K1-D3
 Method BLASTX
 NCBI GI g2213597
 BLAST score 317
 E value 3.0e-29
 Match length 86

% identity	71
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]
Seq. No.	234233
Seq. ID	LIB3272-031-P1-K1-D4
Method	BLASTX
NCBI GI	g728880
BLAST score	181
E value	2.0e-13
Match length	98
% identity	43
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]
Seq. No.	234234
Seq. ID	LIB3272-031-P1-K1-D5
Method	BLASTX
NCBI GI	g495725
BLAST score	603
E value	8.0e-63
Match length	133
% identity	85
NCBI Description	(L25042) acetyl-CoA carboxylase [Medicago sativa]
Seq. No.	234235
Seq. ID	LIB3272-031-P1-K1-D6
Method	BLASTX
NCBI GI	g123620
BLAST score	552
E value	6.0e-57
Match length	114
% identity	96
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir_S14950 heat shock cognate protein 70 - tomato >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate 70 [Lycopersicon esculentum]
Seq. No.	234236
Seq. ID	LIB3272-031-P1-K1-E1
Method	BLASTX
NCBI GI	g3702332
BLAST score	199
E value	2.0e-24
Match length	98
% identity	66
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	234237
Seq. ID	LIB3272-031-P1-K1-E10
Method	BLASTX
NCBI GI	g167367
BLAST score	542
E value	9.0e-56
Match length	119
% identity	89

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No. 234243
 Seq. ID LIB3272-031-P1-K1-F11
 Method BLASTX
 NCBI GI g3913996
 BLAST score 422
 E value 1.0e-41
 Match length 119
 % identity 70

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR
 >gi_2208927_dbj_BAA20482_ (D85610) ATP-dependent protease Lon [Spinacia oleracea]

Seq. No. 234244
 Seq. ID LIB3272-031-P1-K1-F2
 Method BLASTX
 NCBI GI g2267567
 BLAST score 391
 E value 6.0e-38
 Match length 87
 % identity 85

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No. 234245
 Seq. ID LIB3272-031-P1-K1-F3
 Method BLASTX
 NCBI GI g2982311
 BLAST score 250
 E value 2.0e-21
 Match length 92
 % identity 59

NCBI Description (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea mariana]

Seq. No. 234246
 Seq. ID LIB3272-031-P1-K1-F4
 Method BLASTX
 NCBI GI g2811025
 BLAST score 202
 E value 1.0e-19
 Match length 90
 % identity 61

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_ (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 234247
 Seq. ID LIB3272-031-P1-K1-F5
 Method BLASTX
 NCBI GI g2507421
 BLAST score 467
 E value 7.0e-47
 Match length 97

% identity	63
NCBI Description	(L36159) unknown protein [Medicago sativa]
Seq. No.	234253
Seq. ID	LIB3272-031-P1-K1-G6
Method	BLASTX
NCBI GI	g3845257
BLAST score	161
E value	5.0e-11
Match length	100
% identity	6
NCBI Description	(AE001413) predicted integral membrane protein [Plasmodium falciparum]
Seq. No.	234254
Seq. ID	LIB3272-031-P1-K1-G7
Method	BLASTX
NCBI GI	g3142698
BLAST score	509
E value	9.0e-52
Match length	137
% identity	68
NCBI Description	(AF064542) protein farnesyltransferase subunit A [Arabidopsis thaliana]
Seq. No.	234255
Seq. ID	LIB3272-031-P1-K1-H1
Method	BLASTX
NCBI GI	g322750
BLAST score	151
E value	3.0e-11
Match length	77
% identity	56
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]
Seq. No.	234256
Seq. ID	LIB3272-031-P1-K1-H12
Method	BLASTX
NCBI GI	g4539459
BLAST score	400
E value	5.0e-39
Match length	114
% identity	67
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]
Seq. No.	234257
Seq. ID	LIB3272-031-P1-K1-H2
Method	BLASTX
NCBI GI	g3123515
BLAST score	663
E value	8.0e-70
Match length	136
% identity	93
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. ID LIB3272-032-P1-K1-A8
 Method BLASTX
 NCBI GI g2285792
 BLAST score 383
 E value 4.0e-37
 Match length 118
 % identity 64
 NCBI Description (AB004568) cyanase [Arabidopsis thaliana]
 >gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis thaliana]

Seq. No. 234269
 Seq. ID LIB3272-032-P1-K1-B11
 Method BLASTX
 NCBI GI g3158376
 BLAST score 463
 E value 2.0e-46
 Match length 123
 % identity 76
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 234270
 Seq. ID LIB3272-032-P1-K1-B12
 Method BLASTX
 NCBI GI g2677828
 BLAST score 424
 E value 8.0e-42
 Match length 111
 % identity 70
 NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No. 234271
 Seq. ID LIB3272-032-P1-K1-B2
 Method BLASTX
 NCBI GI g3759184
 BLAST score 270
 E value 8.0e-24
 Match length 112
 % identity 53
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 234272
 Seq. ID LIB3272-032-P1-K1-B4
 Method BLASTX
 NCBI GI g3914361
 BLAST score 371
 E value 6.0e-36
 Match length 85
 % identity 80
 NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
 (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
 >gi_2281951_emb_CAB06620_ (Z84822) phospholipase D
 [Nicotiana tabacum]

Seq. No. 234273
 Seq. ID LIB3272-032-P1-K1-B7
 Method BLASTX

NCBI GI g2583134
 BLAST score 179
 E value 3.0e-13
 Match length 105
 % identity 46
 NCBI Description (AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No. 234274
 Seq. ID LIB3272-032-P1-K1-C10
 Method BLASTX
 NCBI GI g1199772
 BLAST score 344
 E value 2.0e-32
 Match length 119
 % identity 62
 NCBI Description (D83226) extensin like protein [Populus nigra]
 >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein [Populus nigra]

Seq. No. 234275
 Seq. ID LIB3272-032-P1-K1-C11
 Method BLASTX
 NCBI GI g1107526
 BLAST score 413
 E value 1.0e-40
 Match length 119
 % identity 66
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 234276
 Seq. ID LIB3272-032-P1-K1-C2
 Method BLASTX
 NCBI GI g1928981
 BLAST score 485
 E value 5.0e-49
 Match length 109
 % identity 89
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 234277
 Seq. ID LIB3272-032-P1-K1-C3
 Method BLASTX
 NCBI GI g4115337
 BLAST score 394
 E value 3.0e-38
 Match length 82
 % identity 16
 NCBI Description (L81141) ubiquitin [Pisum sativum]

Seq. No. 234278
 Seq. ID LIB3272-032-P1-K1-C5
 Method BLASTX
 NCBI GI g543867
 BLAST score 374
 E value 6.0e-36

Method BLASTX
 NCBI GI g629483
 BLAST score 317
 E value 3.0e-29
 Match length 113
 % identity 57
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula pendula]

Seq. No. 234289
 Seq. ID LIB3272-032-P1-K1-E10
 Method BLASTX
 NCBI GI g3901014
 BLAST score 235
 E value 1.0e-19
 Match length 55
 % identity 76
 NCBI Description (AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No. 234290
 Seq. ID LIB3272-032-P1-K1-E11
 Method BLASTX
 NCBI GI g2558962
 BLAST score 360
 E value 2.0e-34
 Match length 96
 % identity 77
 NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No. 234291
 Seq. ID LIB3272-032-P1-K1-E12
 Method BLASTX
 NCBI GI g2244765
 BLAST score 160
 E value 7.0e-11
 Match length 108
 % identity 24
 NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 234292
 Seq. ID LIB3272-032-P1-K1-E2
 Method BLASTX
 NCBI GI g729470
 BLAST score 268
 E value 1.0e-23
 Match length 83
 % identity 63
 NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
 (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
 >gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2)
 precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
 (Z21493) mitochondrial formate dehydrogenase precursor
 [Solanum tuberosum]

Seq. No. 234293
 Seq. ID LIB3272-032-P1-K1-E3
 Method BLASTX
 NCBI GI g401189
 BLAST score 513
 E value 3.0e-52
 Match length 109
 % identity 89
 NCBI Description WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP) (TURGOR-RESPONSIVE PROTEIN 7A) >gi_485511_pir_S33617 trg-31 protein - garden pea >gi_20426_emb_CAA79159_ (Z18288) trg-31 [Pisum sativum]

Seq. No. 234294
 Seq. ID LIB3272-032-P1-K1-E4
 Method BLASTX
 NCBI GI g1076660
 BLAST score 188
 E value 4.0e-14
 Match length 47
 % identity 79
 NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 234295
 Seq. ID LIB3272-032-P1-K1-E9
 Method BLASTX
 NCBI GI g3646373
 BLAST score 596
 E value 5.0e-62
 Match length 116
 % identity 93
 NCBI Description (AJ011078) RGP1 protein [Oryza sativa]

Seq. No. 234296
 Seq. ID LIB3272-032-P1-K1-F11
 Method BLASTX
 NCBI GI g3759184
 BLAST score 285
 E value 2.0e-25
 Match length 125
 % identity 50
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 234297
 Seq. ID LIB3272-032-P1-K1-F12
 Method BLASTX
 NCBI GI g4454097
 BLAST score 277
 E value 1.0e-24
 Match length 67
 % identity 82
 NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]

Seq. No. 234298

Seq. No.	234308
Seq. ID	LIB3272-032-P1-K1-G7
Method	BLASTX
NCBI GI	g1001312
BLAST score	270
E value	8.0e-24
Match length	84
% identity	63
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]
Seq. No.	234309
Seq. ID	LIB3272-032-P1-K1-G9
Method	BLASTX
NCBI GI	g549063
BLAST score	140
E value	7.0e-09
Match length	69
% identity	51
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]
Seq. No.	234310
Seq. ID	LIB3272-032-P1-K1-H1
Method	BLASTX
NCBI GI	g441457
BLAST score	290
E value	3.0e-26
Match length	65
% identity	80
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]
Seq. No.	234311
Seq. ID	LIB3272-032-P1-K1-H11
Method	BLASTX
NCBI GI	g3687243
BLAST score	235
E value	9.0e-20
Match length	59
% identity	78
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]
Seq. No.	234312
Seq. ID	LIB3272-032-P1-K1-H2
Method	BLASTX
NCBI GI	g2501578
BLAST score	489
E value	1.0e-49
Match length	104
% identity	95
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir_S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No. 234313
 Seq. ID LIB3272-032-P1-K1-H5
 Method BLASTX
 NCBI GI g2894599
 BLAST score 533
 E value 1.0e-54
 Match length 115
 % identity 81
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 234314
 Seq. ID LIB3272-032-P1-K1-H6
 Method BLASTX
 NCBI GI g2842486
 BLAST score 331
 E value 6.0e-31
 Match length 105
 % identity 65
 NCBI Description (AL021749) putative protein [Arabidopsis thaliana]

Seq. No. 234315
 Seq. ID LIB3272-032-P1-K1-H8
 Method BLASTX
 NCBI GI g3868758
 BLAST score 412
 E value 2.0e-40
 Match length 99
 % identity 77
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 234316
 Seq. ID LIB3272-033-P1-K1-A1
 Method BLASTX
 NCBI GI g4210948
 BLAST score 470
 E value 3.0e-47
 Match length 99
 % identity 91
 NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 234317
 Seq. ID LIB3272-033-P1-K1-A10
 Method BLASTX
 NCBI GI g3023190
 BLAST score 278
 E value 9.0e-25
 Match length 95
 % identity 64
 NCBI Description 14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685)
 14-3-3 protein [Solanum tuberosum]

Seq. No. 234318
 Seq. ID LIB3272-033-P1-K1-A11
 Method BLASTX
 NCBI GI g1431629
 BLAST score 352

E value 2.0e-33
 Match length 95
 % identity 68
 NCBI Description (X99348) pectinacetylerase precursor [Vigna radiata].

Seq. No. 234319
 Seq. ID LIB3272-033-P1-K1-A2
 Method BLASTX
 NCBI GI g3158376
 BLAST score 425
 E value 6.0e-42
 Match length 118
 % identity 74
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 234320
 Seq. ID LIB3272-033-P1-K1-A4
 Method BLASTX
 NCBI GI g2583108
 BLAST score 227
 E value 9.0e-19
 Match length 91
 % identity 55
 NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 234321
 Seq. ID LIB3272-033-P1-K1-A5
 Method BLASTX
 NCBI GI g464986
 BLAST score 469
 E value 4.0e-47
 Match length 87
 % identity 98
 NCBI Description UBIQUITIN-CONJUGATING ENZYME-E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 234322
 Seq. ID LIB3272-033-P1-K1-A6
 Method BLASTX
 NCBI GI g1666234
 BLAST score 551
 E value 8.0e-57
 Match length 103
 % identity 98
 NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No. 234323

BLAST score 179
E value 4.0e-13
Match length 111
% identity 46
NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 234334
Seq. ID LIB3272-033-P1-K1-C4
Method BLASTX
NCBI GI g1076393
BLAST score 360
E value 2.0e-34
Match length 94
% identity 80
NCBI Description RCI14A protein - Arabidopsis thaliana
>gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis thaliana]

Seq. No. 234335
Seq. ID LIB3272-033-P1-K1-C5
Method BLASTX
NCBI GI g4097579
BLAST score 513
E value 3.0e-52
Match length 105
% identity 91
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 234336
Seq. ID LIB3272-033-P1-K1-C7
Method BLASTX
NCBI GI g4510376
BLAST score 205
E value 3.0e-16
Match length 69
% identity 55
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 234337
Seq. ID LIB3272-033-P1-K1-C8
Method BLASTX
NCBI GI g122770
BLAST score 443
E value 4.0e-44
Match length 112
% identity 79
NCBI Description HEMOGLOBIN II >gi_99509_pir_S13378 hemoglobin II - swamp oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina glauca]

Seq. No. 234338
Seq. ID LIB3272-033-P1-K1-C9
Method BLASTX
NCBI GI g3879192
BLAST score 274
E value 3.0e-24

NCBI GI g2271477
 BLAST score 321
 E value 8.0e-30
 Match length 76
 % identity 84
 NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No. 234355
 Seq. ID LIB3272-033-P1-K1-F6
 Method BLASTX
 NCBI GI g3063449
 BLAST score 336
 E value 1.0e-31
 Match length 90
 % identity 72
 NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]

Seq. No. 234356
 Seq. ID LIB3272-033-P1-K1-G10
 Method BLASTX
 NCBI GI g4335763
 BLAST score 251
 E value 1.0e-21
 Match length 90
 % identity 50
 NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 234357
 Seq. ID LIB3272-033-P1-K1-G11
 Method BLASTX
 NCBI GI g1055130
 BLAST score 238
 E value 4.0e-20
 Match length 118
 % identity 43
 NCBI Description (U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No. 234358
 Seq. ID LIB3272-033-P1-K1-G12
 Method BLASTX
 NCBI GI g1928981
 BLAST score 498
 E value 1.0e-50
 Match length 106
 % identity 93
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 234359
 Seq. ID LIB3272-033-P1-K1-G3
 Method BLASTX
 NCBI GI g1928981
 BLAST score 549

Seq. ID LIB3272-034-P1-K1-A4.
 Method BLASTX
 NCBI GI g3386615
 BLAST score 157
 E value 1.0e-10
 Match length 54
 % identity 63
 NCBI Description (AC004665) putative phosphomannomutase [Arabidopsis thaliana]

Seq. No. 234371
 Seq. ID LIB3272-034-P1-K1-A5
 Method BLASTX
 NCBI GI g3395431
 BLAST score 209
 E value 1.0e-16
 Match length 76
 % identity 49
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 234372
 Seq. ID LIB3272-034-P1-K1-A7
 Method BLASTX
 NCBI GI g549063
 BLAST score 211
 E value 4.0e-17
 Match length 70
 % identity 63
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1072464_pir_A38958 IgE-dependent histamine-releasing
 factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
 21kd polypeptide [Oryza sativa]

Seq. No. 234373
 Seq. ID LIB3272-034-P1-K1-A9
 Method BLASTX
 NCBI GI g419789
 BLAST score 482
 E value 1.0e-48
 Match length 121
 % identity 79
 NCBI Description hypothetical protein - potato

Seq. No. 234374
 Seq. ID LIB3272-034-P1-K1-B1
 Method BLASTX
 NCBI GI g3914430
 BLAST score 491
 E value 8.0e-50
 Match length 98
 % identity 97
 NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
 CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
 >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta
 subunit [Spinacia oleracea]

Seq. No. 234375

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

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Seq. No.      234392
Seq. ID      L1B3272-034-P1-K1-D7
Method       BLASTX
NCBI GI      g2879867
BLAST score   396
E value      1.0e-38
Match length  106
% identity    71
NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]
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Seq. No.      234394
Seq. ID      LIB3272-034-P1-K1-E12
Method       BLASTX
NCBI GI      g1173209
BLAST score   633
E value      2.0e-66
Match length  129
% identity    98
NCBI Description  40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
protein S16 protein - upland cotton
>gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
[Gossypium hirsutum]
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33874

Seq. No. 234396
 Seq. ID LIB3272-034-P1-K1-E6
 Method BLASTX
 NCBI GI g3122673
 BLAST score 412
 E value 2.0e-40
 Match length 112
 % identity 75
 NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447
 (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 234397
 Seq. ID LIB3272-034-P1-K1-E7
 Method BLASTX
 NCBI GI g543867
 BLAST score 369
 E value 2.0e-35
 Match length 104
 % identity 78
 NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
 >gi_1076684_pir_A47493 H+-transporting ATP synthase (EC
 3.6.1.34) gamma chain precursor - sweet potato
 >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gamma subunit
 [Ipomoea batatas]

Seq. No. 234398
 Seq. ID LIB3272-034-P1-K1-E8
 Method BLASTX
 NCBI GI g1332579
 BLAST score 580
 E value 4.0e-60
 Match length 117
 % identity 10
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 234399
 Seq. ID LIB3272-034-P1-K1-E9
 Method BLASTX
 NCBI GI g4220477
 BLAST score 279
 E value 7.0e-25
 Match length 114
 % identity 56
 NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 234400
 Seq. ID LIB3272-034-P1-K1-F10
 Method BLASTX
 NCBI GI g2583134
 BLAST score 243
 E value 1.0e-20
 Match length 123
 % identity 46
 NCBI Description (AC002387) putative proline-rich protein [Arabidopsis
 thaliana]

Seq. No. 234401

BLAST score 158
 E value 5.0e-11
 Match length 45
 % identity 71
 NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 234407
 Seq. ID LIB3272-034-P1-K1-F7
 Method BLASTX
 NCBI GI g3643609
 BLAST score 382
 E value 6.0e-37
 Match length 124
 % identity 63
 NCBI Description (AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No. 234408
 Seq. ID LIB3272-034-P1-K1-F8
 Method BLASTX
 NCBI GI g3928095
 BLAST score 171
 E value 3.0e-12
 Match length 109
 % identity 38
 NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No. 234409
 Seq. ID LIB3272-034-P1-K1-G10
 Method BLASTX
 NCBI GI g3212869
 BLAST score 570
 E value 5.0e-59
 Match length 120
 % identity 87
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 234410
 Seq. ID LIB3272-034-P1-K1-G2
 Method BLASTX
 NCBI GI g3158474
 BLAST score 324
 E value 5.0e-36
 Match length 91
 % identity 89
 NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 234411
 Seq. ID LIB3272-034-P1-K1-G4
 Method BLASTX
 NCBI GI g322750
 BLAST score 615
 E value 3.0e-64
 Match length 120
 % identity 98
 NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco
 >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana

0904010 : 101000

Seq. No. 234417
Seq. ID LIB3272-034-P1-K1-H11

Method BLASTX
 NCBI GI g1928981
 BLAST score 394
 E value 1.0e-38
 Match length 90
 % identity 53
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 234418
 Seq. ID LIB3272-034-P1-K1-H2
 Method BLASTX
 NCBI GI g1332579
 BLAST score 665
 E value 4.0e-70
 Match length 134
 % identity 10
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 234419
 Seq. ID LIB3272-034-P1-K1-H5
 Method BLASTX
 NCBI GI g4103324
 BLAST score 529
 E value 4.0e-54
 Match length 111
 % identity 92
 NCBI Description (AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No. 234420
 Seq. ID LIB3272-034-P1-K1-H6
 Method BLASTX
 NCBI GI g475048
 BLAST score 527
 E value 6.0e-54
 Match length 115
 % identity 58
 NCBI Description (X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana]

Seq. No. 234421
 Seq. ID LIB3272-034-P1-K1-H8
 Method BLASTX
 NCBI GI g585973
 BLAST score 602
 E value 1.0e-62
 Match length 130
 % identity 91
 NCBI Description FRUCTOKINASE >gi_626018_pir_S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283 (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf_2108342A fructokinase [Solanum tuberosum]

Seq. No. 234422
 Seq. ID LIB3272-034-P1-K1-H9
 Method BLASTX

Seq. ID LIB3272-035-P1-K1-A3
 Method BLASTX
 NCBI GI g1709498
 BLAST score 559
 E value 1.0e-57
 Match length 125
 % identity 80
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
 thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
 [Arabidopsis thaliana]

Seq. No. 234426
 Seq. ID LIB3272-035-P1-K1-A6
 Method BLASTX
 NCBI GI g2078350
 BLAST score 606
 E value 4.0e-63
 Match length 138
 % identity 83
 NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 234427
 Seq. ID LIB3272-035-P1-K1-A8
 Method BLASTX
 NCBI GI g133249
 BLAST score 311
 E value 1.0e-28
 Match length 78
 % identity 45
 NCBI Description CHLOROPLAST 33 KD RIBONUCLEOPROTEIN PRECURSOR
 >gi_100390_pir_S12111 ribonucleoprotein, 33K, precursor -
 common tobacco >gi_20005_emb_CAA37879_ (X53932) 33 kDa
 ribonucleoprotein precursor [Nicotiana tabacum]

Seq. No. 234428
 Seq. ID LIB3272-035-P1-K1-A9
 Method BLASTX
 NCBI GI g3894159
 BLAST score 228
 E value 8.0e-19
 Match length 130
 % identity 38
 NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No. 234429
 Seq. ID LIB3272-035-P1-K1-B1
 Method BLASTX
 NCBI GI g1945611
 BLAST score 301
 E value 2.0e-27
 Match length 134
 % identity 45
 NCBI Description (AB003103) 26S proteasome subunit p55 [Homo sapiens]
 >gi_4506221_ref_NP_002807.1_pPSMD12_ proteasome (prosome,
 macropain) 26S subunit, non-ATPase,

Seq. No. 234430
 Seq. ID LIB3272-035-P1-K1-B10
 Method BLASTX
 NCBI GI g119355
 BLAST score 506
 E value 1.0e-51
 Match length 112
 % identity 88
 NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
 >gi_100869_pir_S16257 phosphopyruvate hydratase (EC
 4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
 [Zea mays]

Seq. No. 234431
 Seq. ID LIB3272-035-P1-K1-B12
 Method BLASTX
 NCBI GI g2462929
 BLAST score 486
 E value 5.0e-49
 Match length 144
 % identity 64
 NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No. 234432
 Seq. ID LIB3272-035-P1-K1-B4
 Method BLASTX
 NCBI GI g133867
 BLAST score 371
 E value 9.0e-36
 Match length 91
 % identity 80
 NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal
 protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
 ribosomal protein S11 [Zea mays]

Seq. No. 234433
 Seq. ID LIB3272-035-P1-K1-C2
 Method BLASTX
 NCBI GI g126770
 BLAST score 705
 E value 1.0e-74
 Match length 134
 % identity 100
 NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir_SYCNMU malate
 synthase (EC 4.1.3.2) - upland cotton
 >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
 [Gossypium hirsutum]

Seq. No. 234434
 Seq. ID LIB3272-035-P1-K1-C3
 Method BLASTX
 NCBI GI g548774
 BLAST score 421
 E value 2.0e-41
 Match length 108
 % identity 76

% identity	45
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]
Seq. No.	234444
Seq. ID	LIB3272-035-P1-K1-D8
Method	BLASTX
NCBI GI	g1729971
BLAST score	220
E value	2.0e-18
Match length	109
% identity	51
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa]
Seq. No.	234445
Seq. ID	LIB3272-035-P1-K1-D9
Method	BLASTX
NCBI GI	g2511594
BLAST score	641
E value	3.0e-67
Match length	139
% identity	86
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.	234446
Seq. ID	LIB3272-035-P1-K1-E11
Method	BLASTX
NCBI GI	g419781
BLAST score	138
E value	1.0e-08
Match length	45
% identity	64
NCBI Description	probable cysteine proteinase precursor (clone CYP-7) - common tobacco >gi_19849_emb_CAA78361_ (Z13959) tobacco pre-pro-cysteine proteinase [Nicotiana tabacum]
Seq. No.	234447
Seq. ID	LIB3272-035-P1-K1-E12
Method	BLASTX
NCBI GI	g3421102
BLAST score	392
E value	3.0e-38
Match length	86
% identity	83
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]
Seq. No.	234448
Seq. ID	LIB3272-035-P1-K1-E2
Method	BLASTX

Seq. No. 234478
 Seq. ID LIB3272-036-P1-K1-A7
 Method BLASTX
 NCBI GI g3986695
 BLAST score 645
 E value 9.0e-68
 Match length 139
 % identity 93
 NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No. 234479
 Seq. ID LIB3272-036-P1-K1-A8
 Method BLASTX
 NCBI GI g464986
 BLAST score 493
 E value 7.0e-50
 Match length 92
 % identity 98
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_(Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_(X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1_(AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 234480
 Seq. ID LIB3272-036-P1-K1-B12
 Method BLASTX
 NCBI GI g2146740
 BLAST score 408
 E value 6.0e-40
 Match length 111
 % identity 72
 NCBI Description inner mitochondrial membrane protein - Arabidopsis thaliana
 >gi_603056 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]

Seq. No. 234481
 Seq. ID LIB3272-036-P1-K1-B4
 Method BLASTX
 NCBI GI g4191788
 BLAST score 453
 E value 3.0e-45
 Match length 128
 % identity 65
 NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No. 234482
 Seq. ID LIB3272-036-P1-K1-B5
 Method BLASTX
 NCBI GI g3334123

BLAST score 288
 E value 6.0e-26
 Match length 85
 % identity 74
 NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
 >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of
 mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787
 (AC002334) mitochondrial F1-ATPase, gamma subunit
 [Arabidopsis thaliana]

Seq. No. 234483
 Seq. ID LIB3272-036-P1-K1-B6
 Method BLASTX
 NCBI GI g1172597
 BLAST score 229
 E value 4.0e-19
 Match length 47
 % identity 94
 NCBI Description WOUND-INDUCED BASIC PROTEIN >gi_81888_pir_JS0731
 wound-inducible basic protein - kidney bean >gi_169365
 (L00625) basic protein [Phaseolus vulgaris]
 >gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein
 [Phaseolus vulgaris]

Seq. No. 234484
 Seq. ID LIB3272-036-P1-K1-B7
 Method BLASTX
 NCBI GI g4510363
 BLAST score 523
 E value 2.0e-53
 Match length 110
 % identity 89
 NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis
 thaliana]

Seq. No. 234485
 Seq. ID LIB3272-036-P1-K1-B9
 Method BLASTX
 NCBI GI g2129871
 BLAST score 278
 E value 1.0e-24
 Match length 89
 % identity 62
 NCBI Description proline-rich protein, 14K - kidney bean >gi_1420885
 (U34333) proline-rich 14 kDa protein [Phaseolus vulgaris]

Seq. No. 234486
 Seq. ID LIB3272-036-P1-K1-C10
 Method BLASTX
 NCBI GI g3986695
 BLAST score 616
 E value 2.0e-64
 Match length 135
 % identity 91
 NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No. 234487

Seq. No.	234503
Seq. ID	LIB3272-036-P1-K1-E2
Method	BLASTX
NCBI GI	g3763932
BLAST score	219
E value	9.0e-18
Match length	68
% identity	62
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]
Seq. No.	234504
Seq. ID	LIB3272-036-P1-K1-E4
Method	BLASTX
NCBI GI	g2651310
BLAST score	239
E value	4.0e-20
Match length	129
% identity	35
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]
Seq. No.	234505
Seq. ID	LIB3272-036-P1-K1-E6
Method	BLASTX
NCBI GI	g4204313
BLAST score	160
E value	7.0e-11
Match length	79
% identity	42
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	234506
Seq. ID	LIB3272-036-P1-K1-E7
Method	BLASTX
NCBI GI	g461498
BLAST score	536
E value	6.0e-55
Match length	134
% identity	75
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]
Seq. No.	234507
Seq. ID	LIB3272-036-P1-K1-E8
Method	BLASTX
NCBI GI	g3386621
BLAST score	507
E value	1.0e-51
Match length	118
% identity	81
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 234536
 Seq. ID LIB3272-037-P1-K1-B1
 Method BLASTX
 NCBI GI g3063396
 BLAST score 527
 E value 7.0e-54
 Match length 117
 % identity 85
 NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 234537
 Seq. ID LIB3272-037-P1-K1-B10
 Method BLASTX
 NCBI GI g3450889
 BLAST score 358
 E value 3.0e-34
 Match length 102
 % identity 74
 NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 234538
 Seq. ID LIB3272-037-P1-K1-B12
 Method BLASTX
 NCBI GI g462195
 BLAST score 442
 E value 6.0e-44
 Match length 92
 % identity 93
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 >gi_100682_pir_S21636 GOS2 protein - rice
 >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
 >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 234539
 Seq. ID LIB3272-037-P1-K1-B2
 Method BLASTX
 NCBI GI g730456
 BLAST score 305
 E value 1.0e-41
 Match length 118
 % identity 69
 NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 234540
 Seq. ID LIB3272-037-P1-K1-B3
 Method BLASTX
 NCBI GI g266945
 BLAST score 558
 E value 2.0e-57
 Match length 127
 % identity 87
 NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
 >gi_100065_pir_S19978 ribosomal protein L9 - garden pea
 >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
 >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9 [Pisum sativum]

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Seq. ID LIB3272-037-P1-K1-C9
 Method BLASTX
 NCBI GI g3249084
 BLAST score 266
 E value 2.0e-23
 Match length 103
 % identity 18
 NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No. 234552
 Seq. ID LIB3272-037-P1-K1-D11
 Method BLASTX
 NCBI GI g629670
 BLAST score 288
 E value 7.0e-26
 Match length 95
 % identity 61
 NCBI Description hypothetical protein - tomato

Seq. No. 234553
 Seq. ID LIB3272-037-P1-K1-D2
 Method BLASTX
 NCBI GI g231504
 BLAST score 668
 E value 2.0e-70
 Match length 137
 % identity 96
 NCBI Description ACTIN 100 >gi_100420_pir_S20092 actin - potato (fragment) >gi_1345579_emb_CAA39276_ (X55746) actin [Solanum tuberosum]

Seq. No. 234554
 Seq. ID LIB3272-037-P1-K1-D6
 Method BLASTX
 NCBI GI g3281853
 BLAST score 162
 E value 4.0e-11
 Match length 33
 % identity 94
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 234555
 Seq. ID LIB3272-037-P1-K1-D7
 Method BLASTX
 NCBI GI g3023847
 BLAST score 329
 E value 7.0e-31
 Match length 83
 % identity 80
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No. 234556
 Seq. ID LIB3272-037-P1-K1-D9


```

BLAST score      329
E value         1.0e-30
Match length    79
% identity      82
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
                  (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]

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Seq. No.      234577
Seq. ID       LIB3272-037-P1-K1-G2
Method        BLASTX
NCBI GI       g559684
BLAST score   596
E value       5.0e-62
Match length  131
% identity    89
NCBI Description (L36097) aquaporin [Mesembryanthemum crystallinum]
```

```
Seq. No.      234578
Seq. ID      LIB3272-037-P1-K1-G3
Method       BLASTX
NCBI GI      g3158474
BLAST score   456
E value      1.0e-45
Match length  111
% identity   81
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
```

```
Seq. No.      234579
Seq. ID       LIB3272-037-P1-K1-G4
Method        BLASTX
NCBI GI       g3395436
BLAST score    241
E value        2.0e-20
Match length   97
% identity     46
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      234580
Seq. ID      LIB3272-037-P1-K1-G7
Method       BLASTX
NCBI GI      g2129770
BLAST score   246
E value      6.0e-21
Match length  70
% identity    66
NCBI Description  xyloglucan endotransglycosylase-related protein XTR-2 -
                  Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan
                  endotransglycosylase-related protein [Arabidopsis thaliana]
                  >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan
                  transferase related protein [Arabidopsis thaliana]
```

```
Seq. No.      234581
Seq. ID      LIB3272-037-P1-K1-G8
Method       BLASTX
NCBI GI      q2500047
```



```
Seq. No.      234600
Seq. ID      LIB3272-038=P1-K1-C4
Method       BLASTX
NCBI GI      g3033400
BLAST score   522
E value      3.0e-53
Match length  123
% identity    79
NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
```

Seq. No.	234601
Seq. ID	LIB3272-038-P1-K1-C7
Method	BLASTX
NCBI GI	g3510256
BLAST score	187
E value	5.0e-14
Match length	101
% identity	44
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

```
Seq. No.      234602
Seq. ID      LIB3272-038-P1-K1-C9
Method       BLASTX
NCBI GI      gi1709498
BLAST score   341
E value      3.0e-32
Match length  84
% identity    75
NCBI Description  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
                thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                [Arabidopsis thaliana]
```

```
Seq. No.      234603
Seq. ID       LIB3272-038-P1-K1-D10
Method        BLASTX
NCBI GI       g3337366
BLAST score    368
E value        3.0e-35
Match length   135
% identity     29
NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      234604
Seq. ID      LIB3272-038-P1-K1-D11
Method       BLASTX
NCBI GI      g2500399
BLAST score   475
E value      8.0e-48
Match length 109
% identity   90
NCBI Description 40S RIBOSOMAL PROTEIN S3 >gi_1836060_bbs_179561 (S83098)
ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls,
embryos, Peptide, 253 aa] [Ambystoma mexicanum]
```


E value 9.0e-58
 Match length 121
 % identity 90
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir_JQ1187
 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
 thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
 [Arabidopsis thaliana]

Seq. No. 234611
 Seq. ID LIB3272-038-P1-K1-E2
 Method BLASTX
 NCBI GI g125606
 BLAST score 457
 E value 9.0e-46
 Match length 99
 % identity 88
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248
 pyruvate kinase (EC 2.7.1.40) - potato
 >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
 tuberosum]

Seq. No. 234612
 Seq. ID LIB3272-038-P1-K1-E4
 Method BLASTX
 NCBI GI g2388575
 BLAST score 211
 E value 8.0e-17
 Match length 116
 % identity 39
 NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 234613
 Seq. ID LIB3272-038-P1-K1-E5
 Method BLASTX
 NCBI GI g136636
 BLAST score 560
 E value 9.0e-58
 Match length 106
 % identity 96
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
 LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
 >gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 -
 Arabidopsis thaliana >gi_442594_pdb_1AAK Ubiquitin
 Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK
 Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
 >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
 thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
 [Arabidopsis thaliana]

Seq. No. 234614
 Seq. ID LIB3272-038-P1-K1-E9
 Method BLASTX
 NCBI GI g117988
 BLAST score 265
 E value 3.0e-23
 Match length 74

Seq. ID LIB3272-038-P1-K1-F7
 Method BLASTX
 NCBI GI g4406780
 BLAST score 414
 E value 1.0e-40
 Match length 103
 % identity 75
 NCBI Description (AC006532) putative multispanning membrane protein
 [Arabidopsis thaliana]

Seq. No. 234621
 Seq. ID LIB3272-038-P1-K1-G1
 Method BLASTX
 NCBI GI g2827552
 BLAST score 459
 E value 6.0e-46
 Match length 128
 % identity 51
 NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 234622
 Seq. ID LIB3272-038-P1-K1-G11
 Method BLASTX
 NCBI GI g119350
 BLAST score 387
 E value 1.0e-37
 Match length 86
 % identity 90
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir_JQ1187
 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
 thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
 [Arabidopsis thaliana]

Seq. No. 234623
 Seq. ID LIB3272-038-P1-K1-G12
 Method BLASTX
 NCBI GI g1922278
 BLAST score 227
 E value 3.0e-19
 Match length 48
 % identity 85
 NCBI Description (Z86091) TCTP protein [Fragaria x ananassa]

Seq. No. 234624
 Seq. ID LIB3272-038-P1-K1-G2
 Method BLASTX
 NCBI GI g924951
 BLAST score 156
 E value 2.0e-10
 Match length 47
 % identity 62
 NCBI Description (U30324) class I chitinase [Theobroma cacao]

Seq. No. 234625
 Seq. ID LIB3272-038-P1-K1-G3
 Method BLASTX

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% identity	93
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.	234645
Seq. ID	LIB3272-039-P1-K1-C3
Method	BLASTX
NCBI GI	g117188
BLAST score	261
E value	6.0e-23
Match length	99
% identity	47
NCBI Description	CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2) >gi_81423_pir__A35867 cytochrome P450 71A1 - avocado
Seq. No.	234646
Seq. ID	LIB3272-039-P1-K1-C6
Method	BLASTX
NCBI GI	g167367
BLAST score	571
E value	3.0e-59
Match length	106
% identity	98
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]
Seq. No.	234647
Seq. ID	LIB3272-039-P1-K1-C7
Method	BLASTX
NCBI GI	g2262159
BLAST score	399
E value	4.0e-39
Match length	93
% identity	78
NCBI Description	(AC002329) predicted protein similar to S.pombe protein C5H10.03 [Arabidopsis thaliana]
Seq. No.	234648
Seq. ID	LIB3272-039-P1-K1-C8
Method	BLASTX
NCBI GI	g2129944
BLAST score	333
E value	9.0e-32
Match length	72
% identity	85
NCBI Description	RNA-binding protein RZ-1 - wood tobacco >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1 [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861) RNA binding protein, RZ-1 [Nicotiana sylvestris]
Seq. No.	234649
Seq. ID	LIB3272-039-P1-K1-D10
Method	BLASTX
NCBI GI	g2738949
BLAST score	291
E value	2.0e-26
Match length	104
% identity	57
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x

ananassa]

Seq. No. 234650
 Seq. ID LIB3272-039-P1-K1-D11
 Method BLASTX
 NCBI GI g4206789
 BLAST score 251
 E value 1.0e-21
 Match length 66
 % identity 71
 NCBI Description (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No. 234651
 Seq. ID LIB3272-039-P1-K1-D12
 Method BLASTX
 NCBI GI g4105772
 BLAST score 425
 E value 5.0e-42
 Match length 111
 % identity 43
 NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 234652
 Seq. ID LIB3272-039-P1-K1-D2
 Method BLASTX
 NCBI GI g133249
 BLAST score 160
 E value 5.0e-11
 Match length 47
 % identity 38
 NCBI Description CHLOROPLAST 33 KD RIBONUCLEOPROTEIN PRECURSOR
 >gi_100390_pir_S12111 ribonucleoprotein, 33K, precursor -
 common tobacco >gi_20005_emb_CAA37879 (X53932) 33 kDa
 ribonucleoprotein precursor [Nicotiana tabacum]

Seq. No. 234653
 Seq. ID LIB3272-039-P1-K1-D3
 Method BLASTX
 NCBI GI g3367578
 BLAST score 298
 E value 3.0e-27
 Match length 84
 % identity 68
 NCBI Description (AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 234654
 Seq. ID LIB3272-039-P1-K1-D4
 Method BLASTX
 NCBI GI g3297827
 BLAST score 253
 E value 8.0e-22
 Match length 85
 % identity 65
 NCBI Description (AL031032) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	234660
Seq. ID	LIB3272-039-P1-K1-E10
Method	BLASTX
NCBI GI	g4098128
BLAST score	467
E value	5.0e-47
Match length	102
% identity	89
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.	234661
Seq. ID	LIB3272-039-P1-K1-E11
Method	BLASTX
NCBI GI	g481236
BLAST score	299
E value	4.0e-27
Match length	72
% identity	82
NCBI Description	hypothetical protein - Madagascar periwinkle >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide [Catharanthus roseus]
Seq. No.	234662
Seq. ID	LIB3272-039-P1-K1-E3
Method	BLASTX
NCBI GI	g115492
BLAST score	558
E value	1.0e-57
Match length	110
% identity	54
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]
Seq. No.	234663
Seq. ID	LIB3272-039-P1-K1-E5
Method	BLASTX
NCBI GI	g4572679
BLAST score	182
E value	8.0e-14
Match length	45
% identity	73
NCBI Description	(AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]
Seq. No.	234664
Seq. ID	LIB3272-039-P1-K1-E6
Method	BLASTX
NCBI GI	g508304
BLAST score	208
E value	1.0e-16
Match length	50
% identity	80
NCBI Description	(L22305) corC [Medicago sativa]
Seq. No.	234665
Seq. ID	LIB3272-039-P1-K1-E7


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Method          BLASTX
NCBI GI         g730463
BLAST score     322
E value        7.0e-30
Match length    105
% identity      59
NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
>gi_630323_pir_S44069 ribosomal protein L35a.e.c15 - yeast
(Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
protein L37 [Saccharomyces cerevisiae]
>gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
[Saccharomyces cerevisiae]
```

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Seq. No.      234671
Seq. ID      LIB3272-039-P1-K1-F2
Method       BLASTX
NCBI GI      g548852
BLAST score   301
E value      1.0e-27
Match length  71
% identity    80
NCBI Description  40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal
protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
subunit ribosomal protein [Oryza sativa]
```

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Seq. No.      234672
Seq. ID      LIB3272-039-P1-K1-F3
Method       BLASTX
NCBI GI      g2979544
BLAST score   162
E value      2.0e-11
Match length  92
% identity   40
NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
```

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Seq. No.      234673
Seq. ID      LIB3272-039-P1-K1-F9
Method       BLASTX
NCBI GI      gi20669
BLAST score   445
E value      1.0e-44
Match length  93
% identity    88
NCBI Description  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi_19566_emb_CAA42905 (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
```

Seq. No.	234674
Seq. ID	LIB3272-039-P1-K1-G3
Method	BLASTX
NCBI GI	g549063
BLAST score	316
E value	3.0e-29
Match length	81
% identity	74

0609-7000

0609-7383

0609-7000

0609-7383

0609-7383

Method BLASTX
 NCBI GI g1928981
 BLAST score 525
 E value 1.0e-53
 Match length 117
 % identity 91
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 234705
 Seq. ID LIB3272-040-P1-K1-E1
 Method BLASTX
 NCBI GI g3860277
 BLAST score 397
 E value 5.0e-42
 Match length 129
 % identity 74
 NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 234706
 Seq. ID LIB3272-040-P1-K1-E10
 Method BLASTX
 NCBI GI g4102723
 BLAST score 567
 E value 1.0e-58
 Match length 120
 % identity 70
 NCBI Description (AF015784) TATA-box binding protein [Phaseolus vulgaris]

Seq. No. 234707
 Seq. ID LIB3272-040-P1-K1-E12
 Method BLASTX
 NCBI GI g1173043
 BLAST score 318
 E value 2.0e-29
 Match length 68
 % identity 91
 NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi_479441_pir_S33899 ribosomal protein L38 - tomato (cv. Moneymaker)
 >gi_313027_emb_CAA49599_ (X69979) ribosomal protein L38 [Lycopersicon esculentum]

Seq. No. 234708
 Seq. ID LIB3272-040-P1-K1-E2
 Method BLASTX
 NCBI GI g3063454
 BLAST score 140
 E value 1.0e-08
 Match length 101
 % identity 37
 NCBI Description (AC003981) F22013.16 [Arabidopsis thaliana]

Seq. No. 234709
 Seq. ID LIB3272-040-P1-K1-E4
 Method BLASTX

Seq. ID LIB3272-041-P1-K1-F9
 Method BLASTX
 NCBI GI g2924520
 BLAST score 547
 E value 3.0e-56
 Match length 123
 % identity 86
 NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)
 [Arabidopsis thaliana]

Seq. No. 234745
 Seq. ID LIB3272-041-P1-K1-G11
 Method BLASTX
 NCBI GI g2961085
 BLAST score 110
 E value 3.0e-09
 Match length 96
 % identity 44
 NCBI Description (AF037228) transcription factor [Arabidopsis thaliana]

Seq. No. 234746
 Seq. ID LIB3272-041-P1-K1-G2
 Method BLASTX
 NCBI GI g3608140
 BLAST score 159
 E value 1.0e-10
 Match length 87
 % identity 41
 NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 234747
 Seq. ID LIB3272-041-P1-K1-G3
 Method BLASTX
 NCBI GI g3608485
 BLAST score 502
 E value 5.0e-51
 Match length 101
 % identity 93
 NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No. 234748
 Seq. ID LIB3272-041-P1-K1-H1
 Method BLASTX
 NCBI GI g3024583
 BLAST score 184
 E value 7.0e-14
 Match length 96
 % identity 48
 NCBI Description RT14 PROTEIN HOMOLOG >gi_2347196 (AC002338) RT14 protein
 isolog [Arabidopsis thaliana]

Seq. No. 234749
 Seq. ID LIB3272-041-P1-K1-H2
 Method BLASTX
 NCBI GI g2984709
 BLAST score 385
 E value 3.0e-37

09684016 101000

Match length 80
% identity 90
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 234750
Seq. ID LIB3272-041-P1-K1-H3
Method BLASTX
NCBI GI g3023858
BLAST score 431
E value 1.0e-42
Match length 93
% identity 86
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
PROTEIN >gi_1256608 (U44850) G protein beta subunit
[Glycine max]

Seq. No. 234751
Seq. ID LIB3272-041-P1-K1-H7
Method BLASTX
NCBI GI g4115949
BLAST score 195
E value 3.0e-15
Match length 63
% identity 65
NCBI Description (AF118223) contains similarity to adenosine deaminases
[Arabidopsis thaliana]

Seq. No. 234752
Seq. ID LIB3272-041-P1-K1-H8
Method BLASTX
NCBI GI g1408471
BLAST score 447
E value 2.0e-44
Match length 102
% identity 78
NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis
thaliana] >gi_3851707 (AF102173) actin depolymerizing
factor 1 [Arabidopsis thaliana]

Seq. No. 234753
Seq. ID LIB3272-042-P1-K1-A11
Method BLASTX
NCBI GI g2702376
BLAST score 219
E value 9.0e-18
Match length 89
% identity 46
NCBI Description (AF038605) Similar to acyl-CoA dehydrogenase; coded for by
C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA
yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded
for by C. elegans cDNA yk158e10.3; coded for by C. elegans
cDNA yk427... >gi_4455127_gb_AAD21088_ (AF127558)
isovaleryl-CoA dehydrogenase precursor [Caenorhabditis
elegans]

Seq. No. 234754
Seq. ID LIB3272-042-P1-K1-A12

090301 101000Z

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Seq. No.      234756
Seq. ID      LIB3272-042-P1-K1-A3
Method       BLASTX
NCBI GI      g3980393
BLAST score   375
E value      5.0e-36
Match length  122
% identity    58
NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
```

Seq. No.	234758
Seq. ID	LIB3272-042-P1-K1-A6
Method	BLASTX
NCBI GI	g4406372
BLAST score	439
E value	1.0e-43
Match length	119
% identity	70

Match length	99
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L32
Seq. No.	234770
Seq. ID	LIB3272-042-P1-K1-C11
Method	BLASTX
NCBI GI	g267082
BLAST score	578
E value	7.0e-60
Match length	111
% identity	94
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir_JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]
Seq. No.	234771
Seq. ID	LIB3272-042-P1-K1-C2
Method	BLASTX
NCBI GI	g3860274
BLAST score	152
E value	4.0e-10
Match length	32
% identity	81
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana] >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	234772
Seq. ID	LIB3272-042-P1-K1-C3
Method	BLASTX
NCBI GI	g3037047
BLAST score	491
E value	1.0e-49
Match length	114
% identity	75
NCBI Description	(AF053354) 1-aminocyclopropane-1-carboxylic acid oxidase [Phaseolus vulgaris]
Seq. No.	234773
Seq. ID	LIB3272-042-P1-K1-C4
Method	BLASTX
NCBI GI	g1669585
BLAST score	147
E value	8.0e-12
Match length	60
% identity	50
NCBI Description	(D88649) cytosolic ascorbate peroxidase [Cucumis sativus]
Seq. No.	234774
Seq. ID	LIB3272-042-P1-K1-C6
Method	BLASTX
NCBI GI	g1263291
BLAST score	406
E value	1.0e-60
Match length	118
% identity	99

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 234790
 Seq. ID LIB3272-042-P1-K1-F2
 Method BLASTX
 NCBI GI g3738327
 BLAST score 352
 E value 2.0e-33
 Match length 141
 % identity 50
 NCBI Description (AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 234791
 Seq. ID LIB3272-042-P1-K1-F4
 Method BLASTX
 NCBI GI g487046
 BLAST score 227
 E value 1.0e-18
 Match length 103
 % identity 46
 NCBI Description photosystem I chain II precursor - wood tobacco
 >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
 [Nicotiana sylvestris]

Seq. No. 234792
 Seq. ID LIB3272-042-P1-K1-F5
 Method BLASTX
 NCBI GI g266579
 BLAST score 237
 E value 5.0e-20
 Match length 75
 % identity 61
 NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_169713 (L02306)
 metallothionein [Ricinus communis]

Seq. No. 234793
 Seq. ID LIB3272-042-P1-K1-F7
 Method BLASTX
 NCBI GI g170507
 BLAST score 130
 E value 6.0e-14
 Match length 70
 % identity 59
 NCBI Description (M59251) ORF [Lycopersicon esculentum] >gi_1172167 (U44386)
 heat shock protein [Solanum lycopersicum]

Seq. No. 234794
 Seq. ID LIB3272-042-P1-K1-G1
 Method BLASTX
 NCBI GI g3319882
 BLAST score 716
 E value 5.0e-76
 Match length 141
 % identity 96
 NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No. 234815
 Seq. ID LIB3272-043-P1-K1-C10
 Method BLASTX
 NCBI GI g2244904
 BLAST score 219
 E value 8.0e-18
 Match length 70
 % identity 67
 NCBI Description (Z97339) similar to hypothetical protein C02F5.7 - *Caenorha*
 [*Arabidopsis thaliana*]

Seq. No. 234816
 Seq. ID LIB3272-043-P1-K1-C3
 Method BLASTX
 NCBI GI g430947
 BLAST score 440
 E value 1.0e-43
 Match length 109
 % identity 80
 NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein
 [*Arabidopsis thaliana*]

Seq. No. 234817
 Seq. ID LIB3272-043-P1-K1-C5
 Method BLASTX
 NCBI GI g1082054
 BLAST score 287
 E value 8.0e-26
 Match length 122
 % identity 48
 NCBI Description (Z49859) copper transporter protein [*Arabidopsis thaliana*]

Seq. No. 234818
 Seq. ID LIB3272-043-P1-K1-C6
 Method BLASTX
 NCBI GI g4559358
 BLAST score 186
 E value 6.0e-14
 Match length 58
 % identity 57
 NCBI Description (AC006585) putative steroid binding protein [*Arabidopsis*
thaliana]

Seq. No. 234819
 Seq. ID LIB3272-043-P1-K1-C7
 Method BLASTX
 NCBI GI g3702323
 BLAST score 364
 E value 1.0e-61
 Match length 132
 % identity 82
 NCBI Description (AC005397) unknown protein [*Arabidopsis thaliana*]

Seq. No. 234820
 Seq. ID LIB3272-043-P1-K1-D1
 Method BLASTX

Match length	103
% identity	78
NCBI Description	(L37790) cationic peroxidase [Stylosanthes humilis]
Seq. No.	234842
Seq. ID	LIB3272-043-P1-K1-G2
Method	BLASTX
NCBI GI	g1173218
BLAST score	177
E value	4.0e-13
Match length	86
% identity	49
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.	234843
Seq. ID	LIB3272-043-P1-K1-G3
Method	BLASTX
NCBI GI	g1220196
BLAST score	476
E value	5.0e-48
Match length	97
% identity	94
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.	234844
Seq. ID	LIB3272-043-P1-K1-G4
Method	BLASTX
NCBI GI	g3023847
BLAST score	169
E value	2.0e-12
Match length	42
% identity	76
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]
Seq. No.	234845
Seq. ID	LIB3272-043-P1-K1-G6
Method	BLASTX
NCBI GI	g548852
BLAST score	277
E value	1.0e-24
Match length	82
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S subunit ribosomal protein [Oryza sativa]
Seq. No.	234846
Seq. ID	LIB3272-043-P1-K1-G7
Method	BLASTX
NCBI GI	g3868758
BLAST score	344
E value	1.0e-32
Match length	85

Seq. No.	234852
Seq. ID	LIB3272-044-P1-K1-A1
Method	BLASTX
NCBI GI	g2160166
BLAST score	207
E value	1.0e-16
Match length	105
% identity	51
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.	234853
Seq. ID	LIB3272-044-P1-K1-A10
Method	BLASTX
NCBI GI	g1107526
BLAST score	348
E value	6.0e-33
Match length	100
% identity	66
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]
Seq. No.	234854
Seq. ID	LIB3272-044-P1-K1-A3
Method	BLASTX
NCBI GI	g2129753
BLAST score	201
E value	1.0e-15
Match length	55
% identity	75
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]
Seq. No.	234855
Seq. ID	LIB3272-044-P1-K1-A5
Method	BLASTX
NCBI GI	g1702983
BLAST score	356
E value	7.0e-34
Match length	111
% identity	59
NCBI Description	AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir_S11850 hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034_ (L44142) auxin-repressed protein [Fragaria ananassa]
Seq. No.	234856
Seq. ID	LIB3272-044-P1-K1-A6
Method	BLASTX
NCBI GI	g1419088
BLAST score	686
E value	1.0e-72
Match length	133
% identity	96
NCBI Description	(Z71395) calreticulin [Nicotiana plumbaginifolia]

[Solanum tuberosum]

Seq. No. 234867
 Seq. ID LIB3272-044-P1-K1-C2
 Method BLASTX
 NCBI GI g2982268
 BLAST score 348
 E value 6.0e-33
 Match length 75
 % identity 91
 NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No. 234868
 Seq. ID LIB3272-044-P1-K1-C4
 Method BLASTX
 NCBI GI g3212869
 BLAST score 449
 E value 9.0e-45
 Match length 118
 % identity 69
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 234869
 Seq. ID LIB3272-044-P1-K1-C7
 Method BLASTX
 NCBI GI g481236
 BLAST score 265
 E value 3.0e-23
 Match length 64
 % identity 81
 NCBI Description hypothetical protein - Madagascar periwinkle
 >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide
 [Catharanthus roseus]

Seq. No. 234870
 Seq. ID LIB3272-044-P1-K1-C8
 Method BLASTX
 NCBI GI g2677830
 BLAST score 525
 E value 1.0e-53
 Match length 112
 % identity 93
 NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No. 234871
 Seq. ID LIB3272-044-P1-K1-D1
 Method BLASTX
 NCBI GI g4263712
 BLAST score 302
 E value 1.0e-27
 Match length 80
 % identity 70
 NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 234872

BLAST score 267
E value 1.0e-23
Match length 79
% identity 73
NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No. 234883
Seq. ID LIB3272-044-P1-K1-E8
Method BLASTX
NCBI GI g549063
BLAST score 163
E value 5.0e-17
Match length 70
% identity 71
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No. 234884
Seq. ID LIB3272-044-P1-K1-E9
Method BLASTX
NCBI GI g2462753
BLAST score 150
E value 8.0e-10
Match length 34
% identity 79
NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 234885
Seq. ID LIB3272-044-P1-K1-F1
Method BLASTX
NCBI GI g2995384
BLAST score 233
E value 1.0e-19
Match length 87
% identity 62
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No. 234886
Seq. ID LIB3272-044-P1-K1-F11
Method BLASTX
NCBI GI g266567
BLAST score 202
E value 8.0e-16
Match length 62
% identity 58
NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi_421956_pir_S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato >gi_21493_emb_CAA46990 (X66284) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No. 234887

NCBI GI g549063
 BLAST score 512
 E value 4.0e-52
 Match length 117
 % identity 83..
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1072464_pir_A38958 IgE-dependent histamine-releasing
 factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
 21kd polypeptide [Oryza sativa]

Seq. No. 234893
 Seq. ID LIB3272-044-P1-K1-G5
 Method BLASTX
 NCBI GI g2811025
 BLAST score 277
 E value 1.0e-24
 Match length 94
 % identity 62
 NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
 (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 234894
 Seq. ID LIB3272-044-P1-K1-G8
 Method BLASTX
 NCBI GI g4432840
 BLAST score 192
 E value 1.0e-14
 Match length 82
 % identity 51
 NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 234895
 Seq. ID LIB3272-044-P1-K1-G9
 Method BLASTX
 NCBI GI g1710585
 BLAST score 362
 E value 1.0e-34
 Match length 84
 % identity 85
 NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1143507_emb_CAA63786_
 (X93587) P0 ribosomal protein [Lupinus luteus]

Seq. No. 234896
 Seq. ID LIB3272-044-P1-K1-H11
 Method BLASTX
 NCBI GI g1666228
 BLAST score 263
 E value 2.0e-34
 Match length 91
 % identity 77
 NCBI Description (U76190) actin [Pisum sativum] >gi_1666230 (U76191) actin
 [Pisum sativum] >gi_1724137 (U81046) actin [Pisum sativum]
 >gi_1724139 (U81047) actin [Pisum sativum]

Seq. No. 234897
 Seq. ID LIB3272-044-P1-K1-H12
 Method BLASTX

Seq. ID LIB3272-045-P1-K1-A11
 Method BLASTX
 NCBI GI g2160182
 BLAST score 170
 E value 4.0e-12
 Match length 117
 % identity 39
 NCBI Description (AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203
 come from this gene. [Arabidopsis thaliana]

Seq. No. 234903
 Seq. ID LIB3272-045-P1-K1-A6
 Method BLASTX
 NCBI GI g1173234
 BLAST score 327
 E value 2.0e-30
 Match length 72
 % identity 89
 NCBI Description 40S RIBOSOMAL PROTEIN S25 >gi_481909_pir_S40089 ribosomal
 protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714)
 ribosomal protein S25 [Lycopersicon esculentum]
 >gi_1584836_prf_2123431A ribosomal protein S25
 [Lycopersicon esculentum]

Seq. No. 234904
 Seq. ID LIB3272-045-P1-K1-A8
 Method BLASTX
 NCBI GI g2341034
 BLAST score 508
 E value 7.0e-52
 Match length 103
 % identity 97
 NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No. 234905
 Seq. ID LIB3272-045-P1-K1-B10
 Method BLASTX
 NCBI GI g2970051
 BLAST score 445
 E value 3.0e-44
 Match length 109
 % identity 78
 NCBI Description (AB012110) ARG10 [Vigna radiata]

Seq. No. 234906
 Seq. ID LIB3272-045-P1-K1-B11
 Method BLASTX
 NCBI GI g4539417
 BLAST score 290
 E value 4.0e-26
 Match length 67
 % identity 76
 NCBI Description (AL049171) putative protein [Arabidopsis thaliana]

Seq. No. 234907
 Seq. ID LIB3272-045-P1-K1-B12
 Method BLASTX


```

E value          3.0e-68
Match length     126
% identity       98
NCBI Description (U68461) actin [Striga asiatica]

```

```
Seq. No.      234933
Seq. ID       LIB3272-045-P1-K1-F2
Method        BLASTX
NCBI GI       g729470
BLAST score    400
E value       4.0e-39
Match length   102
% identity     75
NCBI Description  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                  (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
                  (Z21493) mitochondrial formate dehydrogenase precursor
                  [Solanum tuberosum]
```

Seq. No.	234934
Seq. ID	LIB3272-045-P1-K1-F3
Method	BLASTX
NCBI GI	g3080442
BLAST score	317
E value	2.0e-29
Match length	85
% identity	67
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

```

Seq. No.      234935
Seq. ID       LIB3272-045-P1-K1-F5
Method        BLASTX
NCBI GI       g113116
BLAST score    443
E value       5.0e-44
Match length   143
% identity     59
NCBI Description  ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
                >gi_111396_pir_A35007 ATP citrate (pro-S)-lyase (EC
                4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase
                [Rattus norvegicus]

```

```
Seq. No.      234936
Seq. ID       LIB3272-045-P1-K1-F8
Method        BLASTX
NCBI GI       g2369766
BLAST score   198
E value       5.0e-33
Match length  115
% identity    49
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
```

```
Seq. No.      234937
Seq. ID      LIB3272-045-P1-K1-G1
Method      BLASTX
NCBI GI      q136251
```


09584016-101000

% identity 92
NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No. 234948
Seq. ID LIB3272-045-P1-K1-H9
Method BLASTX
NCBI GI g3320120
BLAST score 158
E value 9.0e-11
Match length 98
% identity 34
NCBI Description (U66669) 3-hydroxyisobutyryl-coenzyme A hydrolase [Homo sapiens]

Seq. No. 234949
Seq. ID LIB3272-046-P1-K1-A11
Method BLASTX
NCBI GI g3721540
BLAST score 295
E value 1.0e-26
Match length 104
% identity 63
NCBI Description (D83583) Sulfite Reductase [Nicotiana tabacum]
>gi_3738234_dbj_BAA33796_ (AB010717) sulfite reductase [Nicotiana tabacum]

Seq. No. 234950
Seq. ID LIB3272-046-P1-K1-A12
Method BLASTX
NCBI GI g2388570
BLAST score 149
E value 2.0e-09
Match length 110
% identity 36
NCBI Description (AC000098) YUP8H12.12 [Arabidopsis thaliana]

Seq. No. 234951
Seq. ID LIB3272-046-P1-K1-A2
Method BLASTX
NCBI GI g2191131
BLAST score 188
E value 2.0e-14
Match length 55
% identity 67
NCBI Description (AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]

Seq. No. 234952
Seq. ID LIB3272-046-P1-K1-A4
Method BLASTX
NCBI GI g2924520
BLAST score 500
E value 1.0e-50
Match length 124
% identity 79
NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]


```
Seq. No.          234953
Seq. ID           LIB3272-046-P1-K1-A5
Method            BLASTX
NCBI GI           g1838976
BLAST score       279
E value           9.0e-25
Match length      147
% identity        43
NCBI Description   (X73635) vsf-1 [Lycopersicon esculentum]
```

```
Seq. No.      234954
Seq. ID      LIB3272-046-P1-K1-A6
Method       BLASTX
NCBI GI      g3236253
BLAST score   658
E value      3.0e-69
Match length  143
% identity    85
NCBI Description (AC004684) receptor-like protein kinase [Arabidopsis
thaliana]
```

```
Seq. No.      234955
Seq. ID      LIB3272-046-P1-K1-B1
Method       BLASTX
NCBI GI      g433970
BLAST score   128
E value      9.0e-16
Match length  116
% identity    8
NCBI Description (Z28649) polyubiquitin [Acetabularia cliftonii]
```

Seq. No.	234956
Seq. ID	LIB3272-046-P1-K1-B10
Method	BLASTX
NCBI GI	g1545805
BLAST score	157
E value	4.0e-11
Match length	51
% identity	65
NCBI Description	(D64052) cytochrome P450 like TBP [Nicotiana tabacum]

```
Seq. No.      234957
Seq. ID      LIB3272-046-P1-K1-B11
Method       BLASTX
NCBI GI      g303730
BLAST score   533
E value      2.0e-54
Match length  121
% identity    86
NCBI Description (D12540) GTP-binding protein [Pisum sativum]
               >gi_738933_prf__2001457A GTP-binding protein [Pisum
               sativum]
```

Seq. No.	234958
Seq. ID	LIB3272-046-P1-K1-B12
Method	BLASTX

Method	BLASTX
NCBI GI	g2088651
BLAST score	276
E value	2.0e-24
Match length	125
% identity	41
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]
Seq. No.	234974
Seq. ID	LIB3272-046-P1-K1-D7
Method	BLASTX
NCBI GI	g3901014
BLAST score	234
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]
Seq. No.	234975
Seq. ID	LIB3272-046-P1-K1-D8
Method	BLASTX
NCBI GI	g3915031
BLAST score	453
E value	3.0e-45
Match length	128
% identity	70
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232 (X95988) delta 9 stearyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]
Seq. No.	234976
Seq. ID	LIB3272-046-P1-K1-E1
Method	BLASTX
NCBI GI	g1065515
BLAST score	188
E value	4.0e-14
Match length	79
% identity	44
NCBI Description	(U40420) weak similarity to procollagen alpha chain 1(V) chain [Caenorhabditis elegans]
Seq. No.	234977
Seq. ID	LIB3272-046-P1-K1-E10
Method	BLASTX
NCBI GI	g131754
BLAST score	308
E value	4.0e-28
Match length	126
% identity	46
NCBI Description	PPLZ02 PROTEIN >gi_99973_pir_S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_ (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]

Method BLASTX
 NCBI GI g543905
 BLAST score 392
 E value 5.0e-38
 Match length 125
 % identity 63
 NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
 brassinosteroid-regulated protein [Glycine max]

Seq. No. 234994
 Seq. ID LIB3272-046-P1-K1-H1
 Method BLASTX
 NCBI GI g4539335
 BLAST score 312
 E value 1.0e-28
 Match length 144
 % identity 46
 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 234995
 Seq. ID LIB3272-046-P1-K1-H11
 Method BLASTX
 NCBI GI g3935152
 BLAST score 471
 E value 3.0e-47
 Match length 124
 % identity 69
 NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No. 234996
 Seq. ID LIB3272-046-P1-K1-H12
 Method BLASTX
 NCBI GI g3551838
 BLAST score 521
 E value 3.0e-53
 Match length 120
 % identity 84
 NCBI Description (AF070967) SKP1-like protein [Nicotiana glauca]

Seq. No. 234997
 Seq. ID LIB3272-046-P1-K1-H4
 Method BLASTX
 NCBI GI g1155261
 BLAST score 367
 E value 2.0e-42
 Match length 113
 % identity 82
 NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No. 234998
 Seq. ID LIB3272-046-P1-K1-H5
 Method BLASTX
 NCBI GI g2529229
 BLAST score 441
 E value 9.0e-44
 Match length 106


```
Seq. No.      235004
Seq. ID       LIB3272-047-P1-K1-A7
Method        BLASTX
NCBI GI       g3395423
BLAST score    300
E value       3.0e-27
Match length   117
% identity     56
NCBI Description (AC004683) putative protein kinase [Arabidopsis thaliana]
               >gi_3786023 (AC005499) putative protein kinase [Arabidopsis
               thaliana]
```

```
Seq. No.      235005
Seq. ID      LIB3272-047-P1-K1-A8
Method       BLASTX
NCBI GI      g3319882
BLAST score   496
E value      3.0e-50
Match length  101
% identity    92
NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
arietinum]
```

```
Seq. No.      235006
Seq. ID      LIB3272-047-P1-K1-A9
Method       BLASTX
NCBI GI      g1709498
BLAST score   506
E value      2.0e-51
Match length 109
% identity    83
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
>gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
[Arabidopsis thaliana]
```

Seq. No.	235007
Seq. ID	LIB3272-047-P1-K1-B1
Method	BLASTX
NCBI GI	g2982331
BLAST score	578
E value	6.0e-60
Match length	118
% identity	97
NCBI Description	(AF051251) TAT-binding protein homolog [<i>Picea mariana</i>]

```
Seq. No.      235008
Seq. ID       LIB3272-047-P1-K1-B10
Method        BLASTX
NCBI GI       g1737492
BLAST score    407
E value        6.0e-40
Match length   103
% identity     82
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
```

Seq. No. 235009

E value 9.0e-35
 Match length 100
 % identity 70
 NCBI Description (AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No. 235020
 Seq. ID LIB3272-047-P1-K1-C2
 Method BLASTX
 NCBI GI g4455169
 BLAST score 306
 E value 4.0e-28
 Match length 116
 % identity 53
 NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No. 235021
 Seq. ID LIB3272-047-P1-K1-C3
 Method BLASTX
 NCBI GI g1166450
 BLAST score 295
 E value 1.0e-26
 Match length 63
 % identity 84
 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]

Seq. No. 235022
 Seq. ID LIB3272-047-P1-K1-C7
 Method BLASTX
 NCBI GI g3183207
 BLAST score 371
 E value 1.0e-35
 Match length 119
 % identity 55
 NCBI Description HYPOTHETICAL PROTEIN KIAA0017 >gi_285999_dbj_BAA02805_ (D13642) KIAA0017 [Homo sapiens]

Seq. No. 235023
 Seq. ID LIB3272-047-P1-K1-C8
 Method BLASTX
 NCBI GI g2244979
 BLAST score 402
 E value 3.0e-39
 Match length 118
 % identity 68
 NCBI Description (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No. 235024
 Seq. ID LIB3272-047-P1-K1-D12
 Method BLASTX
 NCBI GI g1172995
 BLAST score 213
 E value 4.0e-17
 Match length 89
 % identity 51

Seq. No.	235029
Seq. ID	LIB3272-047-P1-K1-D6
Method	BLASTX
NCBI GI	g2286153
BLAST score	554
E value	4.0e-57
Match length	112
% identity	99
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.	235030
Seq. ID	LIB3272-047-P1-K1-D7
Method	BLASTX
NCBI GI	g1864017
BLAST score	313
E value	4.0e-55
Match length	123
% identity	89
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.	235031
Seq. ID	LIB3272-047-P1-K1-D8
Method	BLASTX
NCBI GI	g3024020
BLAST score	498
E value	1.0e-50
Match length	104
% identity	89
NCBI Description	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation factor 5A3 [Solanium tuberosum]
Seq. No.	235032
Seq. ID	LIB3272-047-P1-K1-D9
Method	BLASTX
NCBI GI	g4128197
BLAST score	172
E value	3.0e-14
Match length	65
% identity	62
NCBI Description	(U75273) acyl-CoA binding protein [Arabidopsis thaliana]
Seq. No.	235033
Seq. ID	LIB3272-047-P1-K1-E10
Method	BLASTX
NCBI GI	g1313972
BLAST score	294
E value	1.0e-26
Match length	118
% identity	53
NCBI Description	(Z72428) major allergen Mal d1 [Malus domestica]
Seq. No.	235034
Seq. ID	LIB3272-047-P1-K1-E11
Method	BLASTX
NCBI GI	g2935298
BLAST score	622

NCBI GI g167367
 BLAST score 461
 E value 3.0e-46
 Match length 120
 % identity 75
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 235056
 Seq. ID LIB3272-047-P1-K1-H7
 Method BLASTX
 NCBI GI g1922938
 BLAST score 189
 E value 2.0e-14
 Match length 105
 % identity 39
 NCBI Description (AC000106) Similar to Caenorhabditis hypothetical protein C07A9.11 (gb_Z29094). [Arabidopsis thaliana]

Seq. No. 235057
 Seq. ID LIB3272-047-P1-K1-H9
 Method BLASTX
 NCBI GI g1332579
 BLAST score 420
 E value 4.0e-45
 Match length 107
 % identity 9
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 235058
 Seq. ID LIB3272-048-P1-K1-A1
 Method BLASTX
 NCBI GI g232031
 BLAST score 197
 E value 2.0e-15
 Match length 77
 % identity 52
 NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No. 235059
 Seq. ID LIB3272-048-P1-K1-A10
 Method BLASTX
 NCBI GI g1353193
 BLAST score 175
 E value 9.0e-13
 Match length 100
 % identity 45
 NCBI Description O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir_JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No. 235060
 Seq. ID LIB3272-048-P1-K1-A12
 Method BLASTX
 NCBI GI g2499945

Seq. No. 235075
 Seq. ID LIB3272-048-P1-K1-D11
 Method BLASTX
 NCBI GI g4314370
 BLAST score 599
 E value 2.0e-62
 Match length 132
 % identity 85
 NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235076
 Seq. ID LIB3272-048-P1-K1-D12
 Method BLASTX
 NCBI GI g2369714
 BLAST score 651
 E value 2.0e-68
 Match length 129
 % identity 94
 NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 235077
 Seq. ID LIB3272-048-P1-K1-D4
 Method BLASTX
 NCBI GI g629806
 BLAST score 600
 E value 2.0e-62
 Match length 115
 % identity 94
 NCBI Description tubulin beta chain - rice >gi_493725_emb_CAA55912_ (X79367)
 beta tubulin [Oryza sativa]

Seq. No. 235078
 Seq. ID LIB3272-048-P1-K1-D6
 Method BLASTX
 NCBI GI g2827559
 BLAST score 160
 E value 7.0e-11
 Match length 42
 % identity 71
 NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]
 >gi_3292808_emb_CAA19798_ (AL031018) putative protein
 [Arabidopsis thaliana]

Seq. No. 235079
 Seq. ID LIB3272-048-P1-K1-D7
 Method BLASTX
 NCBI GI g3603456
 BLAST score 511
 E value 4.0e-52
 Match length 105
 % identity 30
 NCBI Description (AF088848) polyubiquitin [Capsicum chinense]

Seq. No. 235080
 Seq. ID LIB3272-048-P1-K1-D9
 Method BLASTX


```
BLAST score      658
E value         3.0e-69
Match length    127
% identity      99
NCBI Description translation elongation factor eEF-1 alpha chain - maize
(fragment)
```

Seq. No.	235111
Seq. ID	LIB3272-049-P1-K1-A7
Method	BLASTX
NCBI GI	g1519680
BLAST score	167
E value	1.0e-11
Match length	127
% identity	31
NCBI Description	(U67953) contains similarity to C3HC4-class zinc finger (PS:PS00518) [Caenorhabditis elegans]

```
Seq. No.      235112
Seq. ID       LIB3272-049-P1-K1-A8
Method        BLASTX
NCBI GI       g169913
BLAST score    403
E' value      2.0e-39
Match length   128
% identity     59
NCBI Description (M92090) beta-amylase [Glycine max]
```

```
Seq. No.      235113
Seq. ID      LIB3272-049-P1-K1-B11
Method       BLASTX
NCBI GI      g1888485
BLAST score   435
E value      4.0e-43
Match length  98
% identity    83
NCBI Description (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
```

Seq. No.	235114
Seq. ID	LIB3272-049-P1-K1-B12
Method	BLASTX
NCBI GI	g3643609
BLAST score	414
E value	1.0e-40
Match length	126
% identity	67
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

```
Seq. No.          235115
Seq. ID           LIB3272-049-P1-K1-B2
Method            BLASTX
NCBI GI           g2829133
BLAST score       148
E value           2.0e-09
Match length      102
% identity        35
```


0904016-201000

```
Seq. No.      235117
Seq. ID       LIB3272-049-P1-K1-B6
Method        BLASTX
NCBI GI       g3928099
BLAST score   272
E value       5.0e-24
Match length  122
% identity    24
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      235119
Seq. ID       LIB3272-049-P1-K1-C10
Method        BLASTX
NCBI GI       g3860259
BLAST score    212
E value       5.0e-17
Match length   112
% identity     45
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
```

34019

>gi_282883_pir_S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana]
>gi_2842492_emb_CAA16889 (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 235136
Seq. ID LIB3272-049-P1-K1-E11
Method BLASTX
NCBI GI g3169182
BLAST score 313
E value 7.0e-29
Match length 78
% identity 76
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 235137
Seq. ID LIB3272-049-P1-K1-E12
Method BLASTX
NCBI GI g1173256
BLAST score 535
E value 7.0e-55
Match length 108
% identity 94
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No. 235138
Seq. ID LIB3272-049-P1-K1-E2
Method BLASTX
NCBI GI g3281861
BLAST score 216
E value 2.0e-17
Match length 107
% identity 44
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 235139
Seq. ID LIB3272-049-P1-K1-E4
Method BLASTX
NCBI GI g543905
BLAST score 427
E value 3.0e-42
Match length 103
% identity 82
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No. 235140
Seq. ID LIB3272-049-P1-K1-E5
Method BLASTX
NCBI GI g100525
BLAST score 573
E value 2.0e-59
Match length 115

E value 2.0e-45
 Match length 118
 % identity 80
 NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No. 235146
 Seq. ID LIB3272-049-P1-K1-F9
 Method BLASTX
 NCBI GI g1173256
 BLAST score 567
 E value 1.0e-58
 Match length 108
 % identity 100
 NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No. 235147
 Seq. ID LIB3272-049-P1-K1-G1
 Method BLASTX
 NCBI GI g1657948
 BLAST score 538
 E value 3.0e-55
 Match length 117
 % identity 89
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 235148
 Seq. ID LIB3272-049-P1-K1-G7
 Method BLASTX
 NCBI GI g1495366
 BLAST score 424
 E value 7.0e-42
 Match length 89
 % identity 83
 NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 235149
 Seq. ID LIB3272-049-P1-K1-G8
 Method BLASTX
 NCBI GI g3549691
 BLAST score 431
 E value 1.0e-42
 Match length 98
 % identity 73
 NCBI Description (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No. 235150
 Seq. ID LIB3272-049-P1-K1-H10
 Method BLASTX
 NCBI GI g4210948
 BLAST score 481
 E value 2.0e-48
 Match length 100
 % identity 92


```
E value          2.0e-18
Match length     47
% identity       91
NCBI Description WOUND-INDUCED BASIC PROTEIN >gi_81888_pir__JS0731
                 wound-inducible basic protein - kidney bean >gi_169365
                 (L00625) basic protein [Phaseolus vulgaris]
                 >gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein
                 [Phaseolus vulgaris]

Seq. No.         235157
Seq. ID          LIB3272-050-P1-K1-A12
Method           BLASTX
NCBI GI          g3123271
BLAST score      453
E value          3.0e-45
Match length     105
% identity       82
NCBI Description 40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052)
                 ribosomal protein S6 [Arabidopsis thaliana]
```

```
Seq. No.      235158
Seq. ID      LIB3272-050-P1-K1-A3
Method       BLASTX
NCBI GI      g1155261
BLAST score   523
E value      2.0e-53
Match length 118
% identity   86
NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]
```

```
Seq. No.      235159
Seq. ID       LIB3272-050-P1-K1-A5
Method        BLASTX
NCBI GI       g3687237
BLAST score   349
E value       4.0e-33
Match length  117
% identity    62
NCBI Description (AC005169) putative Cys3His zinc-finger protein
               [Arabidopsis thaliana]
```

```
Seq. No.      235160
Seq. ID      LIB3272-050-P1-K1-A9
Method       BLASTX
NCBI GI      g1928981
BLAST score   527
E value      6.0e-54
Match length  114
% identity    92
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
oleracea var. botrytis]
```

```
Seq. No. 235161
Seq. ID LIB3272-050-P1-K1-B10
Method BLASTX
NCBI GI q2501578
```


E value	1.0e-22
Match length	103
% identity	56
NCBI Description	MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR >gi_1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana]
Seq. No.	235167
Seq. ID	LIB3272-050-P1-K1-B6
Method	BLASTX
NCBI GI	g1172995
BLAST score	235
E value	1.0e-19
Match length	94
% identity	54
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir_S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf_2105193A ribosomal protein L22 [Rattus norvegicus]
Seq. No.	235168
Seq. ID	LIB3272-050-P1-K1-B7
Method	BLASTX
NCBI GI	g125606
BLAST score	431
E value	1.0e-42
Match length	95
% identity	85
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]
Seq. No.	235169
Seq. ID	LIB3272-050-P1-K1-C1
Method	BLASTX
NCBI*GI	g4530585
BLAST score	357
E value	4.0e-34
Match length	85
% identity	74
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]
Seq. No.	235170
Seq. ID	LIB3272-050-P1-K1-C10
Method	BLASTX
NCBI GI	g1709498
BLAST score	506
E value	2.0e-51
Match length	109
% identity	83
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin

[*Arabidopsis thaliana*]

Seq. No. 235171
 Seq. ID LIB3272-050-P1-K1-C11
 Method BLASTX
 NCBI GI g3377797
 BLAST score 458
 E value 7.0e-46
 Match length 118
 % identity 76
 NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara]

Seq. No. 235172
 Seq. ID LIB3272-050-P1-K1-C2
 Method BLASTX
 NCBI GI g1172977
 BLAST score 540
 E value 2.0e-55
 Match length 127
 % identity 83
 NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [*Arabidopsis thaliana*]

Seq. No. 235173
 Seq. ID LIB3272-050-P1-K1-C3
 Method BLASTX
 NCBI GI g1666234
 BLAST score 472
 E value 2.0e-47
 Match length 88
 % identity 100
 NCBI Description (U76193) actin [*Pisum sativum*] >gi_1724143 (U81049) actin [*Pisum sativum*]

Seq. No. 235174
 Seq. ID LIB3272-050-P1-K1-C7
 Method BLASTX
 NCBI GI g3024017
 BLAST score 465
 E value 1.0e-46
 Match length 101
 % identity 92
 NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [*Onobrychis viciifolia*]

Seq. No. 235175
 Seq. ID LIB3272-050-P1-K1-C9
 Method BLASTX
 NCBI GI g2677828
 BLAST score 399
 E value 6.0e-39
 Match length 122


```

% identity                66
NCBI Description          (U93166) cysteine protease [Prunus armeniaca]

Seq. No.                  235176
Seq. ID                   LIB3272-050-P1-K1-D10
Method                    BLASTX
NCBI GI                   g125606
BLAST score               443
E value                   4.0e-44
Match length              94
% identity                88
NCBI Description          PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
                          pyruvate kinase (EC 2.7.1.40) - potato
                          >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
                          tuberosum]

Seq. No.                  235177
Seq. ID                   LIB3272-050-P1-K1-D12
Method                    BLASTX
NCBI GI                   g4559342
BLAST score               137
E value                   9.0e-09
Match length              70
% identity                49
NCBI Description          (AC007087) putative copper methylamine oxidase [Arabidopsis
                          thaliana]

Seq. No.                  235178
Seq. ID                   LIB3272-050-P1-K1-D4
Method                    BLASTX
NCBI GI                   g3694872
BLAST score               429
E value                   2.0e-42
Match length              105
% identity                78
NCBI Description          (AF092547) profilin [Ricinus communis]

Seq. No.                  235179
Seq. ID                   LIB3272-050-P1-K1-D5
Method                    BLASTX
NCBI GI                   g3023930
BLAST score               254
E value                   6.0e-22
Match length              70
% identity                60
NCBI Description          HISTONE DEACETYLASE 1 (HD1) >gi_2654077_gb_AAB87685_
                          (AF032919) histone deacetylase [Strongylocentrotus
                          purpuratus]

Seq. No.                  235180
Seq. ID                   LIB3272-050-P1-K1-D7
Method                    BLASTX
NCBI GI                   g3851636
BLAST score               515
E value                   2.0e-52
Match length              115
% identity                84

```


NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224
translation elongation factor eEF-1 beta' chain - rice
>gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
[Oryza sativa]

Seq. No. 235186
Seq. ID LIB3272-050-P1-K1-E5
Method BLASTX
NCBI GI g3687237
BLAST score 319
E value 1.0e-29
Match length 123
% identity 58
NCBI Description (AC005169) putative Cys3His zinc-finger protein
[Arabidopsis thaliana]

Seq. No. 235187
Seq. ID LIB3272-050-P1-K1-E6
Method BLASTX
NCBI GI g1173187
BLAST score 471
E value 2.0e-47
Match length 109
% identity 83
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir_S56673
ribosomal protein S23.e, cytosolic (clone RJ3) - garden
strawberry >gi_643074 (U19940) putative 40S ribosomal
protein s12 [Fragaria x ananassa]

Seq. No. 235188
Seq. ID LIB3272-050-P1-K1-E7
Method BLASTX
NCBI GI g1928981
BLAST score 549
E value 2.0e-56
Match length 114
% identity 95
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
oleracea var. botrytis]

Seq. No. 235189
Seq. ID LIB3272-050-P1-K1-E9
Method BLASTX
NCBI GI g508304
BLAST score 277
E value 1.0e-24
Match length 66
% identity 79
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 235190
Seq. ID LIB3272-050-P1-K1-F1
Method BLASTX
NCBI GI g2130073
BLAST score 186
E value 5.0e-14
Match length 78


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Match length      109
% identity        52
NCBI Description  (AC000132) No definition line found [Arabidopsis thaliana]
```

```
Seq. No.      235222
Seq. ID      LIB3272-051-P1-K1-C10
Method       BLASTX
NCBI GI      g4335751
BLAST score   394
E value      3.0e-38
Match length  89
% identity   80
NCBI Description (AC006284) putative methyltransferase [Arabidopsis
thaliana]
```

```
Seq. No.      235223
Seq. ID       LIB3272-051-P1-K1-C11
Method        BLASTX
NCBI GI       g1706318
BLAST score   427
E value       3.0e-42
Match length  111
% identity    70
NCBI Description  GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)
                >gi_1362098_pir_S56177 probable glutamate decarboxylase -
                tomato >gi_995555_emb_CAA56812_ (X80840) homology to
                pyroxidal-5'-phosphate-dependant glutamate decarboxylases;
                putative start codon [Lycopersicon esculentum]
```

```
Seq. No.      235225
Seq. ID      LIB3272-051-P1-K1-C3
Method       BLASTX
NCBI GI      g508304
BLAST score   241
E value      2.0e-20
Match length  82
% identity    57
NCBI Description (L22305) corC [Medicago sativa]
```


NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No. 235227
Seq. ID LIB3272-051-P1-K1-C9
Method BLASTX
NCBI GI g3334659
BLAST score 164
E value 2.0e-11
Match length 42
% identity 74

NCBI Description (Y10489) putative cytochrome P450 [Glycine max]

Seq. No. 235228
Seq. ID LIB3272-051-P1-K1-D1
Method BLASTX
NCBI GI g3859606
BLAST score 250
E value 1.0e-21
Match length 52
% identity 87

NCBI Description (AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No. 235229
Seq. ID LIB3272-051-P1-K1-D10
Method BLASTX
NCBI GI g3694872
BLAST score 492
E value 8.0e-50
Match length 118
% identity 80
NCBI Description (AF092547) profilin [Ricinus communis]

Seq. No. 235230
Seq. ID LIB3272-051-P1-K1-D11
Method BLASTX
NCBI GI g3860255
BLAST score 204
E value 5.0e-16
Match length 131
% identity 44
NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235231
Seq. ID LIB3272-051-P1-K1-D12
Method BLASTX
NCBI GI g3953470
BLAST score 142
E value 9.0e-09
Match length 43
% identity 74
NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]

Seq. No. 235232
Seq. ID LIB3272-051-P1-K1-D6


```
Seq. No.      235247
Seq. ID      LIB3272-051-P1-K1-F7
Method       BLASTX
NCBI GI      g3746568
BLAST score   461
E value      4.0e-46
Match length  98
% identity   90
NCBI Description (AF061638) branched-chain alpha-keto acid decarboxylase E1
               beta subunit [Arabidopsis thaliana]
```

```
Seq. No.      235248
Seq. ID       LIB3272-051-P1-K1-G1
Method        BLASTX
NCBI GI       g4105782
BLAST score    422
E value        1.0e-41
Match length   97
% identity     85
NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]
```

```
Seq. No.      235249
Seq. ID      LIB3272-051-P1-K1-G10
Method       BLASTX
NCBI GI      g2499945
BLAST score   373
E value      7.0e-36
Match length 112
% identity    64
NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                DECARBOXYLASE >gi_1076363_pir_S46440 orotate
                phosphoribosyltransferase (EC 2.4.2.10) /
                orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)
                pyrE-F [Arabidopsis thaliana]
```

```
Seq. No.      235250
Seq. ID       LIB3272-051-P1-K1-G11
Method        BLASTX
NCBI GI       g133867
BLAST score   542
E value       1.0e-55
Match length  123
% identity    84
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal
protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
ribosomal protein S11 [Zea mays]
```

```
Seq. No.      235251
Seq. ID      LIB3272-051-P1-K1-G12
Method       BLASTX
NCBI GI      g1170747
BLAST score   388
E value      1.0e-37
Match length  78
```


Seq. No.	235262
Seq. ID	LIB3272-051-P1-K1-H5
Method	BLASTX
NCBI GI	g2879867
BLAST score	418
E value	4.0e-41
Match length	115
% identity	70
NCBI Description	(AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]
Seq. No.	235263
Seq. ID	LIB3272-051-P1-K1-H7
Method	BLASTX
NCBI GI	g1808656
BLAST score	546
E value	4.0e-56
Match length	136
% identity	74
NCBI Description	(Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]
Seq. No.	235264
Seq. ID	LIB3272-051-P1-K1-H8
Method	BLASTX
NCBI GI	g417060
BLAST score	507
E value	1.0e-51
Match length	113
% identity	86
NCBI Description	GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA LIGASE) (GS) >gi_170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi_1094850_prf__2106409A Gln synthetase [Vigna aconitifolia]
Seq. No.	235265
Seq. ID	LIB3272-051-P1-K1-H9
Method	BLASTX
NCBI GI	g1703108
BLAST score	495
E value	4.0e-50
Match length	91
% identity	100
NCBI Description	ACTIN 2/7 >gi_2129525_pir_S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir_S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]
Seq. No.	235266
Seq. ID	LIB3272-052-P1-K1-A1
Method	BLASTX
NCBI GI	g4469175
BLAST score	144
E value	2.0e-09
Match length	73
% identity	45

NCBI GI g2493144
 BLAST score 412
 E value 2.0e-40
 Match length 97
 % identity 57
 NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir_S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No. 235273
 Seq. ID LIB3272-052-P1-K1-A8
 Method BLASTX
 NCBI GI g4455364
 BLAST score 336
 E value 2.0e-31
 Match length 107
 % identity 59
 NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No. 235274
 Seq. ID LIB3272-052-P1-K1-A9
 Method BLASTX
 NCBI GI g4056469
 BLAST score 576
 E value 1.0e-59
 Match length 112
 % identity 100
 NCBI Description (AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No. 235275
 Seq. ID LIB3272-052-P1-K1-B11
 Method BLASTX
 NCBI GI g464981
 BLAST score 438
 E value 2.0e-43
 Match length 84
 % identity 95
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 235276
 Seq. ID LIB3272-052-P1-K1-B12
 Method BLASTX
 NCBI GI g1709498
 BLAST score 515
 E value 2.0e-52
 Match length 112
 % identity 83

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
>gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
[Arabidopsis thaliana]

Seq. No. 235277
Seq. ID LIB3272-052-P1-K1-B2
Method BLASTX
NCBI GI g3319921
BLAST score 267
E value 2.0e-23
Match length 95
% identity 60
NCBI Description (AJ223388) Hev b 3 [Hevea brasiliensis]
>gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3
[Hevea brasiliensis] >gi_3818475 (AF051317) small rubber
particle protein [Hevea brasiliensis]

Seq. No. 235278
Seq. ID LIB3272-052-P1-K1-B3
Method BLASTX
NCBI GI g1076274
BLAST score 295
E value 1.0e-26
Match length 102
% identity 59
NCBI Description cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No. 235279
Seq. ID LIB3272-052-P1-K1-B4
Method BLASTX
NCBI GI g2495155
BLAST score 152
E value 6.0e-10
Match length 112
% identity 39
NCBI Description GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR).
>gi_1694926_dbj_BAA08910_ (D50407) glutamyl-tRNA reductase
[Cucumis sativus]

Seq. No. 235280
Seq. ID LIB3272-052-P1-K1-C10
Method BLASTX
NCBI GI g3377797
BLAST score 282
E value 3.0e-25
Match length 125
% identity 50
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for
by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
H36046; coded for by A. thaliana cDNA T44067; coded for by
A. thaliana cDNA T14056; coded for by A. thaliana cDNA
R90691 [Ara

Seq. No. 235281
Seq. ID LIB3272-052-P1-K1-C12

% identity 78
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
 Seq. No. 235307
 Seq. ID LIB3272-052-P1-K1-F5
 Method BLASTX
 NCBI GI g1168196
 BLAST score 314
 E value 6.0e-29
 Match length 69
 % identity 88
 NCBI Description 14-3-3-LIKE PROTEIN >gi_555974 (U15036) 14-3-3-like protein [Pisum sativum]

Seq. No. 235308
 Seq. ID LIB3272-052-P1-K1-F8
 Method BLASTX
 NCBI GI g2811026
 BLAST score 372
 E value 1.0e-35
 Match length 80
 % identity 89
 NCBI Description TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi_1946375 (U93215) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] >gi_2347204 (AC002338) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]

Seq. No. 235309
 Seq. ID LIB3272-052-P1-K1-G1
 Method BLASTX
 NCBI GI g3894186
 BLAST score 294
 E value 1.0e-26
 Match length 116
 % identity 53
 NCBI Description (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]

Seq. No. 235310
 Seq. ID LIB3272-052-P1-K1-G10
 Method BLASTX
 NCBI GI g4210948
 BLAST score 571
 E value 5.0e-59
 Match length 109
 % identity 97
 NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 235311
 Seq. ID LIB3272-052-P1-K1-G11
 Method BLASTX
 NCBI GI g4263712
 BLAST score 388
 E value 1.0e-37
 Match length 93
 % identity 77
 NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis

096646-10-100000

NCBI GI	2661840
BLAST score	371
E value	1.0e-35
Match length	96
% identity	70
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.	235318
Seq. ID	LIB3272-052-P1-K1-H10
Method	BLASTX
NCBI GI	g4417280
BLAST score	265
E value	3.0e-23
Match length	70
% identity	77
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]
Seq. No.	235319
Seq. ID	LIB3272-052-P1-K1-H11
Method	BLASTX
NCBI GI	g417148
BLAST score	403
E value	2.0e-39
Match length	130
% identity	61
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir_A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.	235320
Seq. ID	LIB3272-052-P1-K1-H3
Method	BLASTX
NCBI GI	g113621
BLAST score	439
E value	1.0e-43
Match length	102
% identity	86
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366 (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A cytoplasmic aldolase [Zea mays]
Seq. No.	235321
Seq. ID	LIB3272-052-P1-K1-H4
Method	BLASTX
NCBI GI	g266936
BLAST score	397
E value	1.0e-38
Match length	113
% identity	74
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir_A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

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Seq. No.	235328
Seq. ID	LIB3272-053-P1-K1-A4
Method	BLASTX
NCBI GI	g2500354
BLAST score	683
E value	4.0e-72
Match length	132
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

```
Seq. No.      235330
Seq. ID      LIB3272-053-P1-K1-A7
Method       BLASTX
NCBI GI      g4217999
BLAST score   475
E value      9.0e-48
Match length  116
% identity    81
NCBI Description (AC006135) putative ubiquitin--protein ligase
               (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
```

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Seq. No.      235331
Seq. ID      LIB3272-053-P1-K1-A8
Method       BLASTX
NCBI GI      g3885515
BLAST score   388
E value      9.0e-38
Match length  77
% identity    95
NCBI Description: (AF084202) similar to ribosomal protein S26 [Medicago
                  sativa]
```

34061

Seq. ID LIB3272-053-P1-K1-B12
 Method BLASTX
 NCBI GI g541816
 BLAST score 177
 E value 4.0e-13
 Match length 60
 % identity 62
 NCBI Description protein kinase - common ice plant >gi_457689_emb_CAA82990_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No. 235333
 Seq. ID LIB3272-053-P1-K1-B2
 Method BLASTX
 NCBI GI g2499945
 BLAST score 367
 E value 3.0e-35
 Match length 112
 % identity 63
 NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir_S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No. 235334
 Seq. ID LIB3272-053-P1-K1-B4
 Method BLASTX
 NCBI GI g1928981
 BLAST score 297
 E value 4.0e-32
 Match length 113
 % identity 69
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 235335
 Seq. ID LIB3272-053-P1-K1-B5
 Method BLASTX
 NCBI GI g1170747
 BLAST score 380
 E value 1.0e-36
 Match length 86
 % identity 85
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345 (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235336
 Seq. ID LIB3272-053-P1-K1-B6
 Method BLASTX
 NCBI GI g2462763
 BLAST score 148
 E value 2.0e-09
 Match length 54

0964-016-101000

Seq. No.	235341
Seq. ID	LIB3272-053-P1-K1-C4
Method	BLASTX
NCBI GI	g3738283
BLAST score	402
E value	3.0e-39
Match length	82
% identity	85
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

```
Seq. No.      235342
Seq. ID      LIB3272-053-P1-K1-C6
Method       BLASTX
NCBI GI      g4454479
BLAST score   176
E value      1.0e-12
Match length  40
% identity    82
NCBI Description (AC006234) putative riboflavin synthase alpha chain
               [Arabidopsis thaliana]
```

```
Seq. No.      235343
Seq. ID      LIB3272-053-P1-K1-C7
Method       BLASTX
NCBI GI      g4538945
BLAST score   533
E value      1.0e-54
Match length  134
% identity    74
NCBI Description (AL049483) putative thioredoxin [Arabidopsis thaliana]
```

```
Seq. No.      235344
Seq. ID      LIB3272-053-P1-K1-D1
Method       BLASTX
NCBI GI      g3986750
BLAST score   190
E value      9.0e-25
Match length  92
% identity    66
NCBI Description (AF107464) serine/threonine protein phosphatase type 2A
               [Hevea brasiliensis]
```

```
Seq. No.      235345
Seq. ID      LIB3272-053-P1-K1-D6
Method       BLASTX
NCBI GI      g2662310
BLAST score   331
E value      6.0e-31
Match length  116
% identity    62
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
```

Seq. No.	235346
Seq. ID	LIB3272-053-P1-K1-D7

NCBI Description (U81287) glycine-rich RNA-binding protein PsGRBP [Pisum sativum]

```
Seq. No.          235366
Seq. ID           LIB3272-053-P1-K1-G6
Method            BLASTX
NCBI GI           g3935167
BLAST score       334
E value           2.0e-31
Match length      82
% identity        83
NCBI Description   (AC004557) F17L21.10
```

```
Seq. No.      235367
Seq. ID       LIB3272-053-P1-K1-G7
Method        BLASTX
NCBI GI       g303730
BLAST score    187
E value       4.0e-14
Match length   79
% identity     59
NCBI Description (D12540) GTP-binding protein [Pisum sativum]
                >gi_738933_prf__2001457A GTP-binding protein [Pisum
                sativum]
```

```
Seq. No.      235368
Seq. ID      LIB3272-053-P1-K1-H4
Method       BLASTX
NCBI GI      g2924509
BLAST score   199
E value      2.0e-15
Match length  91
% identity    46
NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis
thaliana]
```

```
Seq. No.      235369
Seq. ID      LIB3272-053-P1-K1-H6
Method       BLASTX
NCBI GI      g3367522
BLAST score   315
E value      5.0e-29
Match length  93
% identity    62
NCBI Description (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]
```

```
Seq. No.      235370
Seq. ID       LIB3272-053-P1-K1-H8
Method        BLASTX
NCBI GI       g2529665
BLAST score   .572
E value       4.0e-59
Match length  140
% identity    81
NCBI Description (AC002535) putative ribosomal protein L7A [Arabidopsis
thaliana]
```


Seq. No. 235371
 Seq. ID LIB3272-054-P1-K1-A1
 Method BLASTX
 NCBI GI g126770
 BLAST score 141
 E value 3.0e-09
 Match length 59
 % identity 49
 NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate synthase (EC 4.1.3.2) - upland cotton
 >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
 [Gossypium hirsutum]

Seq. No. 235372
 Seq. ID LIB3272-054-P1-K1-A10
 Method BLASTX
 NCBI GI g508304
 BLAST score 215
 E value 3.0e-17
 Match length 73
 % identity 60
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 235373
 Seq. ID LIB3272-054-P1-K1-A11
 Method BLASTX
 NCBI GI g2792297
 BLAST score 197
 E value 2.0e-15
 Match length 55
 % identity 60
 NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 235374
 Seq. ID LIB3272-054-P1-K1-A2
 Method BLASTX
 NCBI GI g167367
 BLAST score 436
 E value 3.0e-43
 Match length 123
 % identity 68
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 235375
 Seq. ID LIB3272-054-P1-K1-A5
 Method BLASTX
 NCBI GI g3759184
 BLAST score 331
 E value 6.0e-31
 Match length 135
 % identity 52
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 235376
 Seq. ID LIB3272-054-P1-K1-B10
 Method BLASTX

NCBI GI	g625509
BLAST score	602
E value	1.0e-62
Match length	121
% identity	25
NCBI Description	ubiquitin precursor - Arabidopsis thaliana (fragment)
Seq. No.	235377
Seq. ID	LIB3272-054-P1-K1-B2
Method	BLASTX
NCBI GI	g464707
BLAST score	648
E value	4.0e-68
Match length	135
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	235378
Seq. ID	LIB3272-054-P1-K1-B4
Method	BLASTX
NCBI GI	g2764574
BLAST score	503
E value	4.0e-51
Match length	138
% identity	70
NCBI Description	(AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]
Seq. No.	235379
Seq. ID	LIB3272-054-P1-K1-B5
Method	BLASTX
NCBI GI	g4090257
BLAST score	293
E value	1.0e-40
Match length	91
% identity	96
NCBI Description	(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
Seq. No.	235380
Seq. ID	LIB3272-054-P1-K1-B7
Method	BLASTX
NCBI GI	g2244797
BLAST score	166
E value	1.0e-11

Match length	61
% identity	56
NCBI Description	(297336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	235381
Seq. ID	LIB3272-054-P1-K1-B9
Method	BLASTX
NCBI GI	g4090257
BLAST score	286
E value	8.0e-40
Match length	91
% identity	95
NCBI Description	(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
Seq. No.	235382
Seq. ID	LIB3272-054-P1-K1-C1
Method	BLASTX
NCBI GI	g1545805
BLAST score	207
E value	2.0e-16
Match length	71
% identity	63
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]
Seq. No.	235383
Seq. ID	LIB3272-054-P1-K1-C11
Method	BLASTX
NCBI GI	g1419090
BLAST score	389
E value	1.0e-37
Match length	121
% identity	64
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]
Seq. No.	235384
Seq. ID	LIB3272-054-P1-K1-C2
Method	BLASTX
NCBI GI	g3337356
BLAST score	228
E value	7.0e-19
Match length	90
% identity	64
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]
Seq. No.	235385
Seq. ID	LIB3272-054-P1-K1-C3
Method	BLASTX
NCBI GI	g1724100
BLAST score	255
E value	2.0e-22
Match length	70
% identity	70
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]
Seq. No.	235386

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Method	BLASTX
NCBI GI	g4539292
BLAST score	452
E value	4.0e-45
Match length	96
% identity	86
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]
Seq. No.	235397
Seq. ID	LIB3272-054-P1-K1-E3
Method	BLASTX
NCBI GI	g2815246
BLAST score	225
E value	2.0e-18
Match length	55
% identity	73
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]
Seq. No.	235398
Seq. ID	LIB3272-054-P1-K1-E7
Method	BLASTX
NCBI GI	g2129495
BLAST score	274
E value	3.0e-24
Match length	54
% identity	89
NCBI Description	fiber protein E6 (clone SIE6-2A) - sea-island cotton >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090 (U30508) E6 [Gossypium barbadense]
Seq. No.	235399
Seq. ID	LIB3272-054-P1-K1-E9
Method	BLASTX
NCBI GI	g549063
BLAST score	367
E value	4.0e-35
Match length	112
% identity	65
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]
Seq. No.	235400
Seq. ID	LIB3272-054-P1-K1-F11
Method	BLASTX
NCBI GI	g3450889
BLAST score	253
E value	9.0e-22
Match length	60
% identity	80
NCBI Description	(AF083890) 19S proteasome subunit 9 [Arabidopsis thaliana]
Seq. No.	235401
Seq. ID	LIB3272-054-P1-K1-F4
Method	BLASTX

% identity	55
NCBI Description	(Y11987) FPF1 protein [Sinapis alba]
Seq. No.	235407
Seq. ID	LIB3272-054-P1-K1-G10
Method	BLASTX
NCBI GI	g3860277
BLAST score	400
E value	5.0e-39
Match length	95
% identity	82
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.	235408
Seq. ID	LIB3272-054-P1-K1-G3
Method	BLASTX
NCBI GI	g4519673
BLAST score	696
E value	1.0e-73
Match length	140
% identity	83
NCBI Description	(AB017694) WREBP-2 [Nicotiana tabacum]
Seq. No.	235409
Seq. ID	LIB3272-054-P1-K1-G8
Method	BLASTX
NCBI GI	g4204793
BLAST score	636
E value	1.0e-66
Match length	135
% identity	47
NCBI Description	(U52079) P-glycoprotein [Solanum tuberosum]
Seq. No.	235410
Seq. ID	LIB3272-054-P1-K1-G9
Method	BLASTX
NCBI GI	g3158372
BLAST score	436
E value	2.0e-43
Match length	90
% identity	53
NCBI Description	(AF035383) polyubiquitin [Arabidopsis thaliana]
Seq. No.	235411
Seq. ID	LIB3272-054-P1-K1-H1
Method	BLASTX
NCBI GI	g120669
BLAST score	497
E value	2.0e-50
Match length	99
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde

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Seq. No.      235413
Seq. ID       LIB3272-054-P1-K1-H12
Method        BLASTX
NCBI GI       : g3860247
BLAST score   396
E value       2.0e-39
Match length  100
% identity    84
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      235415
Seq. ID      LIB3272-054-P1-K1-H9
Method       BLASTX
NCBI GI      g120777
BLAST score   159
E value      9.0e-11
Match length  75
% identity    44
NCBI Description  SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)
>gi_147901 (M88334) succinic semialdehyde dehydrogenase
[Escherichia coli] >gi_1789015 (AE000351)
succinate-semialdehyde dehydrogenase, NADP-dependent
activity [Escherichia coli]
```

34078

Seq. No. 235417
 Seq. ID LIB3272-055-P1-K1-A12
 Method BLASTX
 NCBI GI g629483
 BLAST score 228
 E value 9.0e-19
 Match length 115
 % identity 44
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula
 pendula]

Seq. No. 235418
 Seq. ID LIB3272-055-P1-K1-A3
 Method BLASTX
 NCBI GI g2982452
 BLAST score 250
 E value 1.0e-21
 Match length 113
 % identity 7
 NCBI Description (AL022223) receptor protein kinase-like protein
 [Arabidopsis thaliana]

Seq. No. 235419
 Seq. ID LIB3272-055-P1-K1-A5
 Method BLASTX
 NCBI GI g862931
 BLAST score 341
 E value 3.0e-32
 Match length 103
 % identity 68
 NCBI Description (U27179) acidic glucanase [Medicago sativa subsp. sativa]

Seq. No. 235420
 Seq. ID LIB3272-055-P1-K1-A6
 Method BLASTX
 NCBI GI g2462762
 BLAST score 341
 E value 4.0e-32
 Match length 126
 % identity 57
 NCBI Description (AC002292) Highly similar to auxin-induced protein
 (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 235421
 Seq. ID LIB3272-055-P1-K1-A7
 Method BLASTX
 NCBI GI g3915826
 BLAST score 456
 E value 1.0e-45
 Match length 119
 % identity 74
 NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 235422

Match length 76
 % identity 91
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
 (M88324) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167347 (M37697) Lea5-A late
 embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235439
 Seq. ID LIB3272-055-P1-K1-D2
 Method BLASTX
 NCBI GI g3281853
 BLAST score 181
 E value 3.0e-13
 Match length 37
 % identity 95
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 235440
 Seq. ID LIB3272-055-P1-K1-D5
 Method BLASTX
 NCBI GI g3482980
 BLAST score 326
 E value 3.0e-30
 Match length 140
 % identity 51
 NCBI Description (AL031369) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235441
 Seq. ID LIB3272-055-P1-K1-D7
 Method BLASTX
 NCBI GI g3241945
 BLAST score 192
 E value 1.0e-14
 Match length 109
 % identity 39
 NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]

Seq. No. 235442
 Seq. ID LIB3272-055-P1-K1-E1
 Method BLASTX
 NCBI GI g167367
 BLAST score 406
 E value 1.0e-39
 Match length 109
 % identity 72
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 235443
 Seq. ID LIB3272-055-P1-K1-E10
 Method BLASTX
 NCBI GI g1621268
 BLAST score 379
 E value 1.0e-36
 Match length 114
 % identity 69
 NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 235458
 Seq. ID LIB3272-055-P1-K1-G9
 Method BLASTX
 NCBI GI g2739168
 BLAST score 311
 E value 2.0e-36
 Match length 115
 % identity 67
 NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No. 235459
 Seq. ID LIB3272-055-P1-K1-H1
 Method BLASTX
 NCBI GI g4455207
 BLAST score 440
 E value 1.0e-43
 Match length 95
 % identity 91
 NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 235460
 Seq. ID LIB3272-055-P1-K1-H10
 Method BLASTX
 NCBI GI g1076737
 BLAST score 414
 E value 8.0e-41
 Match length 81
 % identity 98
 NCBI Description beta-tubulin R1623 - rice

Seq. No. 235461
 Seq. ID LIB3272-055-P1-K1-H7
 Method BLASTX
 NCBI GI g4455207
 BLAST score 339
 E value 8.0e-32
 Match length 96
 % identity 75
 NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 235462
 Seq. ID LIB3272-055-P1-K1-H8
 Method BLASTX
 NCBI GI g544437
 BLAST score 374
 E value 6.0e-36
 Match length 85
 % identity 86
 NCBI Description GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
 >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]

Seq. No. 235463
 Seq. ID LIB3272-055-P1-K1-H9
 Method BLASTX
 NCBI GI g3851636

Seq. ID LIB3272-058-P1-K1-A2
 Method BLASTX
 NCBI GI g1705812
 BLAST score 475
 E value 9.0e-48
 Match length 141
 % identity 64
 NCBI Description ACIDIC CHITINASE PRECURSOR >gi_1150686_emb_CAA92207_ (Z68123) acidic chitinase [Vitis vinifera]

Seq. No. 235468
 Seq. ID LIB3272-058-P1-K1-A3
 Method BLASTX
 NCBI GI g1170747
 BLAST score 385
 E value 3.0e-37
 Match length 87
 % identity 85
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345 (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235469
 Seq. ID LIB3272-058-P1-K1-A4
 Method BLASTX
 NCBI GI g2500347
 BLAST score 254
 E value 2.0e-26
 Match length 117
 % identity 60
 NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG >gi_3878691_emb_CAA90127 (Z49911) similar to ribosomal protein (L7AE family); cDNA EST EMBL:D73957 comes from this gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393 comes from this gene; cD

Seq. No. 235470
 Seq. ID LIB3272-058-P1-K1-A5
 Method BLASTX
 NCBI GI g136636
 BLAST score 543
 E value 9.0e-56
 Match length 105
 % identity 95
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No. 235471

0966-016-10100

Seq. No.	235503
Seq. ID	LIB3272-058-P1-K1-F10
Method	BLASTX
NCBI GI	g2995384
BLAST score	300
E value	2.0e-27
Match length	90
% identity	67
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

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Seq. No.      235504
Seq. ID      LIB3272-058-P1-K1-F11
Method       BLASTX
NCBI GI      g418596
BLAST score   242
E value      2.0e-20
Match length  99
% identity    43
NCBI Description  PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W
                >gi_485540_pir_S33911 hypothetical protein YHR148w - yeast
                (Saccharomyces cerevisiae) >gi_4014_emb_CAA49237 (X69480)
                uORF1 [Saccharomyces cerevisiae] >gi_500654 (U10397)
                Yhr148wp [Saccharomyces cerevisiae]
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Seq. No.          235505
Seq. ID           LIB3272-058-P1-K1-F12
Method            BLASTX
NCBI GI           g1666228
BLAST score       672
E value           7.0e-71
Match length      126
% identity        99
NCBI Description   (U76190) actin [Pisum sativum] >gi_1666230 (U76191) actin
                  [Pisum sativum] >gi_1724137 (U81046) actin [Pisum sativum]
                  >gi_1724139 (U81047) actin [Pisum sativum]
```

```
Seq. No.      235506
Seq. ID       LIB3272-058-P1-K1-F3
Method        BLASTX
NCBI GI       g1657948
BLAST score   492
E value       9.0e-50
Match length  125
% identity    78
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
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Seq. No.      235517
Seq. ID      LIB3272-058-P1-K1-G9
Method       BLASTX
NCBI GI      g2160166
BLAST score   332
E value      5.0e-31
Match length  131
% identity    57
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
```

```
Seq. No.      235518
Seq. ID      LIB3272-058-P1-K1-H1
Method       BLASTX
NCBI GI      g2462929
BLAST score   330
E value      8.0e-31
Match length  135
% identity    56
NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]
```

```
Seq. No.      235519
Seq. ID      LIB3272-058-P1-K1-H10
Method       BLASTX
NCBI GI      g2970051
BLAST score   502
E value      6.0e-51
Match length  107
% identity    90
NCBI Description (AB012110) ARG10 [Vigna radiata].
```

```
Seq. No.      235520
Seq. ID       LIB3272-058-P1-K1-H11
Method        BLASTX
NCBI GI       g4426565
BLAST score   140
E value       3.0e-10
Match length  123
% identity    31
NCBI Description (AF031483) unknown [Rattus norvegicus]
```

```
Seq. No.      235521
Seq. ID      LIB3272-058-P1-K1-H12
Method       BLASTX
NCBI GI      g1173104
BLAST score   447
E value      2.0e-44
Match length  94
% identity    78
NCBI Description  RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease
                  [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease,
                  RNS2 [Arabidopsis thaliana]
```

```
Seq. No.      235522
Seq. ID      LIB3272-058-P1-K1-H2
Method       BLASTX
NCBI GI      g4185140
BLAST score  406
```


E value	1.0e-39
Match length	88
% identity	91
NCBI Description	(AC005724) putative small nuclear ribonucleoprotein E (snRNP-E) [Arabidopsis thaliana]
Seq. No.	235523
Seq. ID	LIB3272-058-P1-K1-H3
Method	BLASTX
NCBI GI	g135406
BLAST score	507
E value	2.0e-51
Match length	99
% identity	96
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir_A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.	235524
Seq. ID	LIB3272-058-P1-K1-H4
Method	BLASTX
NCBI GI	g1730843
BLAST score	187
E value	5.0e-14
Match length	140
% identity	14
NCBI Description	HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION >gi_2131945_pir_S63228 hypothetical protein YNL255c - yeast (Saccharomyces cerevisiae) >gi_1255963_emb_CAA65489_ (X96722) ORF N0852 [Saccharomyces cerevisiae] >gi_1302303_emb_CAA96162_ (Z71531) ORF YNL255c [Saccharomyces cerevisiae]
Seq. No.	235525
Seq. ID	LIB3272-058-P1-K1-H5
Method	BLASTX
NCBI GI	g3882081
BLAST score	685
E value	2.0e-72
Match length	139
% identity	39
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]
Seq. No.	235526
Seq. ID	LIB3272-058-P1-K1-H6
Method	BLASTX
NCBI GI	g1076660
BLAST score	229
E value	6.0e-19
Match length	47
% identity	89
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. ID uC-gsflmaxxa001c12b1
 Method BLASTX
 NCBI GI g3355483
 BLAST score 298
 E value 4.0e-27
 Match length 59
 % identity 81
 NCBI Description (AC004218) gibberellin-regulated protein (GASA5)-like [Arabidopsis thaliana]

Seq. No. 235533
 Seq. ID uC-gsflmaxxa001d12b1
 Method BLASTX
 NCBI GI g2894558
 BLAST score 246
 E value 5.0e-21
 Match length 121
 % identity 60
 NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

Seq. No. 235534
 Seq. ID uC-gsflmaxxa001f01b1
 Method BLASTX
 NCBI GI g1922246
 BLAST score 190
 E value 2.0e-14
 Match length 105
 % identity 42
 NCBI Description (Y10086) putative dehydrogenase [Arabidopsis thaliana]

Seq. No. 235535
 Seq. ID uC-gsflmaxxa001f05b1
 Method BLASTX
 NCBI GI g3402690
 BLAST score 153
 E value 3.0e-10
 Match length 101
 % identity 40
 NCBI Description (AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No. 235536
 Seq. ID uC-gsflmaxxa001f12b1
 Method BLASTX
 NCBI GI g3522937
 BLAST score 234
 E value 9.0e-20
 Match length 77
 % identity 61
 NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 235537
 Seq. ID uC-gsflmaxxa001h05b1
 Method BLASTX
 NCBI GI g3776015
 BLAST score 241
 E value 2.0e-20

NCBI Description (AC000104) Similar to Nicotiana lesion-inducing ORF
(gb_U66269). [Arabidopsis thaliana]

Seq. No. 235559
Seq. ID uC-gsflmaxxa003e12b1
Method BLASTX
NCBI GI g2582665
BLAST score 499
E value 8.0e-51
Match length 105
% identity 94
NCBI Description (Z82983) thi [Citrus sinensis]

Seq. No. 235560
Seq. ID uC-gsflmaxxa003f01b1
Method BLASTX
NCBI GI g3452263
BLAST score 358
E value 3.0e-34
Match length 99
% identity 70
NCBI Description (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis thaliana]

Seq. No. 235561
Seq. ID uC-gsflmaxxa003f02b1
Method BLASTX
NCBI GI g3738257
BLAST score 191
E value 1.0e-14
Match length 42
% identity 95
NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No. 235562
Seq. ID uC-gsflmaxxa003f03b1
Method BLASTX
NCBI GI g3892059
BLAST score 272
E value 5.0e-24
Match length 76
% identity 59
NCBI Description (AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No. 235563
Seq. ID uC-gsflmaxxa003f08b1
Method BLASTX
NCBI GI g3618343
BLAST score 369
E value 3.0e-35
Match length 148
% identity 47
NCBI Description (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]
>gi_4506223_ref_NP_002808.1_pPSMD13_ proteasome (prosome, macropain) 26S subunit, non-ATPase,


```
Seq. No.      235564
Seq. ID       uC-gsflmaxxa003g03b1
Method        BLASTX
NCBI GI       g4580388
BLAST score    224
E value        3.0e-18
Match length   130
% identity     43
NCBI Description (AC007171) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      235565
Seq. ID       uC-gsflmaxxa003g08b1
Method        BLASTX
NCBI GI       g4033424
BLAST score   363
E value       8.0e-35
Match length  82
% identity    87
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
pyrophosphatase [Zea mays]
```

```
Seq. No.      235566
Seq. ID       uC-gsflmaxxa003g10b1
Method        BLASTX
NCBI GI       g3582002
BLAST score   153
E value       5.0e-10
Match length  94
% identity    40
NCBI Description (AJ010943) tomato invertase inhibitor [Lycopersicon
esculentum]
```

```
Seq. No.      235567
Seq. ID       uC-gsflmaxxa003h11b1
Method        BLASTX
NCBI GI       g4432839
BLAST score   355
E value       9.0e-34
Match length  78
% identity    46
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
```

Seq. No.	235568
Seq. ID	uC-gsflmaxxa004d06b1
Method	BLASTX
NCBI GI	g4220524
BLAST score	180
E value	2.0e-13
Match length	40
% identity	78
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	235569
Seq. ID	uC-gsflmaxxa004e02b1
Method	BLASTX

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235580
Seq. ID uC-gsflmaxxa005c05b1
Method BLASTX
NCBI GI g2842490
BLAST score 276
E value 6.0e-25
Match length 71
% identity 70

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 235581
Seq. ID uC-gsflmaxxa005d04b1
Method BLASTX
NCBI GI g3249095
BLAST score 230
E value 4.0e-19
Match length 69
% identity 67

NCBI Description (AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb_L13703 from Schizosaccharomyces pombe. ESTs gb_N37567 and gb_T43002 come from this gene. [Arabidopsis thaliana]

Seq. No. 235582
Seq. ID uC-gsflmaxxa005d08b1
Method BLASTX
NCBI GI g897638
BLAST score 278
E value 8.0e-25
Match length 56
% identity 96

NCBI Description (M10124) unknown protein [Nicotiana tabacum]
>gi_224349_prf__1102209C ORF 3 [Nicotiana sp.]

Seq. No. 235583
Seq. ID uC-gsflmaxxa006a04b1
Method BLASTX
NCBI GI g2880049
BLAST score 391
E value 4.0e-38
Match length 97
% identity 76

NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235584
Seq. ID uC-gsflmaxxa006a07b1
Method BLASTX
NCBI GI g4522012
BLAST score 406
E value 1.0e-39
Match length 111
% identity 70

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235585

Match length 67
 % identity 67
 NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine
 S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
 >gi_2129919_pir_S65957
 5-methyltetrahydropteroyltriglutamate--homocysteine
 S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
 >gi_886471_emb_CAA58474_ (X83499) methionine synthase
 [Catharanthus roseus]

Seq. No. 235591
 Seq. ID uC-gsflmaxxa009a12b1
 Method BLASTX
 NCBI GI g124712
 BLAST score 375
 E value 5.0e-36
 Match length 91
 % identity 73
 NCBI Description BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1 PRECURSOR
 (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) (CELL WALL
 BETA-FRUCTOSIDASE 1) >gi_100159_pir_JQ0991
 beta-fructofuranosidase (EC 3.2.1.26) precursor - carrot
 >gi_167551 (M58362). beta-fructosidase [Daucus carota]

Seq. No. 235592
 Seq. ID uC-gsflmaxxa009b09b1
 Method BLASTX
 NCBI GI g4263787
 BLAST score 212
 E value 5.0e-17
 Match length 92
 % identity 46
 NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]

Seq. No. 235593
 Seq. ID uC-gsflmaxxa009b12b1
 Method BLASTX
 NCBI GI g4455301
 BLAST score 243
 E value 9.0e-21
 Match length 71
 % identity 75
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 235594
 Seq. ID uC-gsflmaxxa009c04b1
 Method BLASTX
 NCBI GI g441457
 BLAST score 335
 E value 2.0e-31
 Match length 74
 % identity 88
 NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
 esculentum]

Seq. No. 235595
 Seq. ID uC-gsflmaxxa009c07b1

BLAST score 252
 E value 1.0e-21
 Match length 56
 % identity 86
 NCBI Description EUKARYOTIC INITIATION FACTOR 4A-15 (EIF-4A-15)
 >gi_485945_emb_CAA55739_ (X79138) NeIF-4A15 [Nicotiana
 tabacum]

Seq. No. 235601
 Seq. ID uC-gsflmaxxa009e08b1
 Method BLASTX
 NCBI GI g3822223
 BLAST score 309
 E value 6.0e-29
 Match length 70
 % identity 79
 NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase E1
 alpha subunit [Arabidopsis thaliana]

Seq. No. 235602
 Seq. ID uC-gsflmaxxa009f01b1
 Method BLASTX
 NCBI GI g2618686
 BLAST score 193
 E value 4.0e-15
 Match length 70
 % identity 47
 NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235603
 Seq. ID uC-gsflmaxxa009f03b1
 Method BLASTX
 NCBI GI g267075
 BLAST score 412
 E value 2.0e-40
 Match length 82
 % identity 89
 NCBI Description TUBULIN BETA-2 CHAIN >gi_388254_emb_CAA38614_ (X54845)
 beta-tubulin 2 [Pisum sativum]

Seq. No. 235604
 Seq. ID uC-gsflmaxxa009f06b1
 Method BLASTX
 NCBI GI g1419758
 BLAST score 357
 E value 2.0e-34
 Match length 75
 % identity 84
 NCBI Description (X98795) geranylgeranyl pyrophosphate synthase [Sinapis
 alba]

Seq. No. 235605
 Seq. ID uC-gsflmaxxa009f09b1
 Method BLASTX
 NCBI GI g2344887
 BLAST score 292
 E value 2.0e-26

retrovirus receptor [Rattus norvegicus]

```
Seq. No.      235626
Seq. ID       uC-gsflmaxxa015b07b1
Method        BLASTX
NCBI GI       g4335773
BLAST score    151
E value       8.0e-10
Match length   91
% identity     42
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      235627
Seq. ID       uC-gsflmaxxa015b09b1
Method        BLASTX
NCBI GI       g2623298
BLAST score   310
E value       2.0e-28
Match length  134
% identity    62
NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]
```

```
Seq. No.      235628
Seq. ID       uC-gsflmaxxa015c03b1
Method        BLASTX
NCBI GI       g3080415
BLAST score    182
E value       6.0e-14
Match length   60
% identity     62
NCBI Description (AL022604) cysteine proteinase - like protein [Arabidopsis
thaliana]
```

Seq. No.	235629
Seq. ID	uC-gsflmaxxa015f04b1
Method	BLASTX
NCBI GI	g130172
BLAST score	190
E value	6.0e-15
Match length	37
% identity	95
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH PHOSPHORYLASE L) >gi_168276 (M64362) starch phosphorylase [Ipomoea batatas]

```
Seq. No.          235630
Seq. ID           uC-gsflmaxxa015f11b1
Method            BLASTX
NCBI GI           g322641
BLAST score       322
E value           3.0e-30
Match length      86
% identity        63
NCBI Description  beta-1,3-glucanase homolog (clone A6) - rape (fragment)
                  >gi_17738_emb_CAA49513_ (X69887) beta-1,3-glucanase
                  homologue [Brassica napus]
```


Seq. No. 235631
 Seq. ID uC-gsflmaxxa026a11b1
 Method BLASTX
 NCBI GI g4056507
 BLAST score 147
 E value 9.0e-10
 Match length 65
 % identity 54
 NCBI Description (AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No. 235632
 Seq. ID uC-gsflmaxxa026b01b1
 Method BLASTX
 NCBI GI g3080391
 BLAST score 238
 E value 4.0e-20
 Match length 75
 % identity 61
 NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 235633
 Seq. ID uC-gsflmaxxa026c01b1
 Method BLASTX
 NCBI GI g1652164
 BLAST score 333
 E value 3.0e-31
 Match length 111
 % identity 61
 NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 235634
 Seq. ID uC-gsflmaxxa026e03b1
 Method BLASTX
 NCBI GI g3150405
 BLAST score 208
 E value 8.0e-17
 Match length 82
 % identity 51
 NCBI Description (AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 235635
 Seq. ID uC-gsflmaxxa026f01b1
 Method BLASTX
 NCBI GI g2661412
 BLAST score 223
 E value 1.0e-18
 Match length 60
 % identity 75
 NCBI Description (AJ000728) MAP kinase kinase [Lycopersicon esculentum]

Seq. No. 235636
 Seq. ID uC-gsflmaxxa026g02b1
 Method BLASTX
 NCBI GI g3914826


```

BLAST score      586
E value         8.0e-61
Match length    128
% identity      81
NCBI Description DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR
>gi_2330560_emb_CAA69972_(Y08722) chloroplast
single-subunit DNA-dependent RNA polymerase [Arabidopsis
thaliana] >gi_2330564_emb_CAA69717_(Y08463) chloroplast
single-subunit DNA-dependent RNA polymerase [Arabidopsis
thaliana] >gi_4115372 (AC005967) chloroplast single subunit
DNA-dependent RNA polymerase [Arabidopsis thaliana]

```

Seq. No.	235637
Seq. ID	uC-gsflmaxxa026g12b1
Method	BLASTX
NCBI GI	g2760837
BLAST score	237
E value	6.0e-20
Match length	110
% identity	38
NCBI Description	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]

```
Seq. No.      235638
Seq. ID       uC-gsflmaxxa026h03b1
Method        BLASTX
NCBI GI       g4539351
BLAST score    183
E value       5.0e-14
Match length   68
% identity     44
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      235639
Seq. ID       uC-gsflmaxxa026h06b1
Method        BLASTX
NCBI GI       g3080396
BLAST score    501
E value        8.0e-51
Match length   136
% identity     69
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      235640
Seq. ID       uC-gsflmaxxa026h11b1
Method        BLASTX
NCBI GI       g3859570
BLAST score   327
E value       2.0e-30
Match length  143
% identity    50
NCBI Description (AF098753) unknown [Oryza sativa]
```

```
Seq. No.      235641
Seq. ID.      uC-gsflmaxxa027a08b1
Method        BLASTX
NCBI GI       g1297187
BLAST score   240
```


NCBI GI g3297824
 BLAST score 161
 E value 3.0e-11
 Match length 82
 % identity 49
 NCBI Description (AL031032) bZIP transcription factor - like protein
 [Arabidopsis thaliana]

Seq. No. 235663
 Seq. ID uC-gsflmaxxa029d09b1
 Method BLASTX
 NCBI GI g3128228
 BLAST score 337
 E value 7.0e-32
 Match length 72
 % identity 89
 NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis
 thaliana] >gi_3337376 (AC004481) putative ribosomal protein
 L18A [Arabidopsis thaliana]

Seq. No. 235664
 Seq. ID uC-gsflmaxxa029d10b1
 Method BLASTX
 NCBI GI g2495256
 BLAST score 564
 E value 3.0e-58
 Match length 121
 % identity 89
 NCBI Description STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 HOMOLOG (HMG
 PROTEIN) >gi_481756_pir_S39242 HMG protein - Madagascar
 periwinkle >gi_433872_emb_CAA82251_ (Z28410) HMG protein
 [Catharanthus roseus]

Seq. No. 235665
 Seq. ID uC-gsflmaxxa029e03b1
 Method BLASTX
 NCBI GI g2760836
 BLAST score 291
 E value 1.0e-26
 Match length 90
 % identity 68
 NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis
 thaliana]

Seq. No. 235666
 Seq. ID uC-gsflmaxxa029e06b1
 Method BLASTX
 NCBI GI g1171642
 BLAST score 187
 E value 1.0e-14
 Match length 45
 % identity 80
 NCBI Description PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
 >gi_481206_pir_S38326 protein kinase - Arabidopsis
 thaliana >gi_166809 (L07248) protein kinase [Arabidopsis
 thaliana]

NCBI Description (297336) CCAAT-binding transcription factor subunit
A(CBF-A) [Arabidopsis thaliana]

Seq. No. 235704
Seq. ID uC-gsflmaxxa040e07b1
Method BLASTX
NCBI GI g3183445
BLAST score 299
E value 4.0e-27
Match length 140
% identity 46

NCBI Description HYPOTHETICAL 30.8 KD PROTEIN IN PPHB-RPOS INTERGENIC REGION
>gi_882629 (U29579) ORF_o302 [Escherichia coli] >gi_1789092
(AE000357) putative dehydrogenase [Escherichia coli]

Seq. No. 235705
Seq. ID uC-gsflmaxxa040e09b1
Method BLASTX
NCBI GI g3056595
BLAST score 247
E value 3.0e-21
Match length 103
% identity 50

NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]

Seq. No. 235706
Seq. ID uC-gsflmaxxa040f01b1
Method BLASTX
NCBI GI g3892059
BLAST score 529
E value 5.0e-54
Match length 146
% identity 71

NCBI Description (AC002330) predicted protein of unknown function
[Arabidopsis thaliana]

Seq. No. 235707
Seq. ID uC-gsflmaxxa040f05b1
Method BLASTX
NCBI GI g2191175
BLAST score 450
E value 8.0e-45
Match length 141
% identity 61

NCBI Description (AF007270) A_IG002P16.24 gene product [Arabidopsis
thaliana]

Seq. No. 235708
Seq. ID uC-gsflmaxxa040g09b1
Method BLASTX
NCBI GI g3881189
BLAST score 419
E value 3.0e-41
Match length 96
% identity 77

NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST
EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337

comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No. 235709
Seq. ID uC-gsflmaxxa040h08b1
Method BLASTX
NCBI GI g1483228
BLAST score 139
E value 1.0e-08
Match length 31
% identity 81
NCBI Description (X99653) MADS3 protein [Betula pendula]

Seq. No. 235710
Seq. ID uC-gsflmaxxa040h10b1
Method BLASTX
NCBI GI g4240385
BLAST score 302
E value 1.0e-27
Match length 122
% identity 52
NCBI Description (AF061027) omega-3 fatty acid desaturase precursor [Vernicia fordii]

Seq. No. 235711
Seq. ID uC-gsflmaxxa041a05b1
Method BLASTX
NCBI GI g1763279
BLAST score 543
E value 1.0e-55
Match length 141
% identity 70
NCBI Description (U73657) tryptophan decarboxylase [Camptotheca acuminata]

Seq. No. 235712
Seq. ID uC-gsflmaxxa041a08b1
Method BLASTX
NCBI GI g1351856
BLAST score 617
E value 2.0e-64
Match length 128
% identity 95
NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

Seq. No. 235713
Seq. ID uC-gsflmaxxa041a09b1
Method BLASTX
NCBI GI g1707032
BLAST score 305
E value 7.0e-28
Match length 126
% identity 32
NCBI Description (U80445) coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for

00000000000000000000

34140

E value 4.0e-27
 Match length 108
 % identity 56
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
 >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 235741
 Seq. ID uC-gsflmaxxa043b07b1
 Method BLASTX
 NCBI GI g4455293
 BLAST score 248
 E value 2.0e-21
 Match length 68
 % identity 74
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 235742
 Seq. ID uC-gsflmaxxa043b09b1
 Method BLASTX
 NCBI GI g557474
 BLAST score 154
 E value 4.0e-10
 Match length 99
 % identity 35
 NCBI Description (U15179) ORF1 [Bacteroides ovatus]

Seq. No. 235743
 Seq. ID uC-gsflmaxxa043e10b1
 Method BLASTX
 NCBI GI g4432835
 BLAST score 200
 E value 1.0e-15
 Match length 83
 % identity 45
 NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 235744
 Seq. ID uC-gsflmaxxa043f02b1
 Method BLASTX
 NCBI GI g2623298
 BLAST score 323
 E value 7.0e-30
 Match length 75
 % identity 76
 NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No. 235745
 Seq. ID uC-gsflmaxxa043f07b1
 Method BLASTX
 NCBI GI g2760830
 BLAST score 228
 E value 8.0e-19
 Match length 99
 % identity 45
 NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis

0365019-1000

Match length 92
 % identity 79
 NCBI Description (Y10116) signal recognition particle subunit 14
 [Arabidopsis thaliana]

Seq. No. 235777
 Seq. ID uC-gsflmaxxa047c10b1
 Method BLASTX
 NCBI GI g4544445
 BLAST score 617
 E value 2.0e-64
 Match length 148
 % identity 82
 NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate
 1-phosphotransferase [Arabidopsis thaliana]

Seq. No. 235778
 Seq. ID uC-gsflmaxxa047e03b1
 Method BLASTX
 NCBI GI g4469023
 BLAST score 560
 E value 1.0e-57
 Match length 128
 % identity 83
 NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 235779
 Seq. ID uC-gsflmaxxa047e06b1
 Method BLASTX
 NCBI GI g3935152
 BLAST score 237
 E value 5.0e-20
 Match length 55
 % identity 80
 NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No. 235780
 Seq. ID uC-gsflmaxxa047f04b1
 Method BLASTX
 NCBI GI g4335731
 BLAST score 160
 E value 8.0e-11
 Match length 126
 % identity 31
 NCBI Description (AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No. 235781
 Seq. ID uC-gsflmaxxa047f05b1
 Method BLASTX
 NCBI GI g3062801
 BLAST score 477
 E value 4.0e-48
 Match length 120
 % identity 75
 NCBI Description (AB012873) arginine decarboxylase [Nicotiana sylvestris]

Seq. No. 235782

Method BLASTX
 NCBI GI g3885338
 BLAST score 179
 E value 6.0e-13
 Match length 80
 % identity 39
 NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 235793
 Seq. ID uC-gsflmaxxa048e05b1
 Method BLASTX
 NCBI GI g3098603
 BLAST score 175
 E value 2.0e-12
 Match length 111
 % identity 33
 NCBI Description (AF052191) katanin p60 subunit [Strongylocentrotus purpuratus]

Seq. No. 235794
 Seq. ID uC-gsflmaxxa048e07b1
 Method BLASTX
 NCBI GI g1621268
 BLAST score 221
 E value 4.0e-18
 Match length 60
 % identity 70
 NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 235795
 Seq. ID uC-gsflmaxxa048f06b1
 Method BLASTX
 NCBI GI g4038030
 BLAST score 382
 E value 8.0e-37
 Match length 151
 % identity 50
 NCBI Description (AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No. 235796
 Seq. ID uC-gsflmaxxa048f11b1
 Method BLASTX
 NCBI GI g2065531
 BLAST score 320
 E value 7.0e-30
 Match length 60
 % identity 92
 NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No. 235797
 Seq. ID uC-gsflmaxxa048g05b1
 Method BLASTX
 NCBI GI g4158232
 BLAST score 581
 E value 4.0e-60
 Match length 128

Match length 71
 % identity 58
 NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato
 >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
 [Solanum tuberosum]

Seq. No. 235803
 Seq. ID uC-gsflmaxxa049c04b1
 Method BLASTX
 NCBI GI g1161926
 BLAST score 161
 E value 4.0e-11
 Match length 50
 % identity 62
 NCBI Description (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
 max]

Seq. No. 235804
 Seq. ID uC-gsflmaxxa049c07b1
 Method BLASTX
 NCBI GI g3128209
 BLAST score 236
 E value 6.0e-20
 Match length 68
 % identity 66
 NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No. 235805
 Seq. ID uC-gsflmaxxa049c11b1
 Method BLASTX
 NCBI GI g2662343
 BLAST score 441
 E value 6.0e-44
 Match length 85
 % identity 100
 NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 235806
 Seq. ID uC-gsflmaxxa049d07b1
 Method BLASTX
 NCBI GI g4580389
 BLAST score 404
 E value 1.0e-39
 Match length 94
 % identity 82
 NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 235807
 Seq. ID uC-gsflmaxxa049d09b1
 Method BLASTX
 NCBI GI g1497987
 BLAST score 161
 E value 4.0e-11
 Match length 74
 % identity 47
 NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]

Seq. No. 235808
 Seq. ID uC-gsflmaxxa049e08b1
 Method BLASTX
 NCBI GI g2117725
 BLAST score 206
 E value 2.0e-16
 Match length 44
 % identity 84
 NCBI Description 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform
 SBE2.2 precursor - Arabidopsis thaliana (fragment)
 >gi_726490 (U22428) starch branching enzyme class II
 [Arabidopsis thaliana]

Seq. No. 235809
 Seq. ID uC-gsflmaxxa049e09b1
 Method BLASTX
 NCBI GI g136107
 BLAST score 204
 E value 4.0e-16
 Match length 104
 % identity 44
 NCBI Description TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL
 AMINOPEPTIDASE) >gi_1082875_pir_S54376
 tripeptidyl-peptidase II (EC 3.4.14.10) - human >gi_339880
 (M73047) tripeptidyl peptidase II [Homo sapiens]
 >gi_4507657_ref_NP_003282.1_pTPP2_ tripeptidyl peptidase II

Seq. No. 235810
 Seq. ID uC-gsflmaxxa049e10b1
 Method BLASTX
 NCBI GI g4455329
 BLAST score 505
 E value 2.0e-51
 Match length 109
 % identity 86
 NCBI Description (AL035525) lysine-ketoglutarate reductase/saccharopine
 [Arabidopsis thaliana]

Seq. No. 235811
 Seq. ID uC-gsflmaxxa049f01b1
 Method BLASTX
 NCBI GI g1346705
 BLAST score 246
 E value 4.0e-21
 Match length 86
 % identity 52
 NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
 >gi_1085765_pir_S40123 endopolygalacturonase (EC 3.2.1.15)
 - Prunus persica >gi_436420_emb_CAA54150_ (X76735)
 endopolygalacturonase [Prunus persica]

Seq. No. 235812
 Seq. ID uC-gsflmaxxa049f03b1
 Method BLASTX
 NCBI GI g4335722
 BLAST score 283
 E value 9.0e-26

Seq. No.	235818
Seq. ID	uC-gsflmaxxa054a08b1
Method	BLASTX
NCBI GI	g3386614
BLAST score	247
E value	3.0e-21
Match length	58
% identity	35
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]
Seq. No.	235819
Seq. ID	uC-gsflmaxxa054a12b1
Method	BLASTX
NCBI GI	g4455202
BLAST score	261
E value	7.0e-23
Match length	65
% identity	77
NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]
Seq. No.	235820
Seq. ID	uC-gsflmaxxa054b12b1
Method	BLASTX
NCBI GI	g3688189
BLAST score	382
E value	3.0e-37
Match length	92
% identity	80
NCBI Description	(AL031804) putative protein kinase [Arabidopsis thaliana]
Seq. No.	235821
Seq. ID	uC-gsflmaxxa054c02b1
Method	BLASTX
NCBI GI	g128592
BLAST score	383
E value	6.0e-37
Match length	99
% identity	71
NCBI Description	POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR >gi_82190_pir_S22495 pollen-specific protein precursor - common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen specific protein [Nicotiana tabacum]
Seq. No.	235822
Seq. ID	uC-gsflmaxxa054c10b1
Method	BLASTX
NCBI GI	g2832625
BLAST score	230
E value	3.0e-19
Match length	97
% identity	52
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]
Seq. No.	235823
Seq. ID	uC-gsflmaxxa054e05b1

% identity	80
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]
Seq. No.	235855
Seq. ID	uC-gsflmaxxa058a09b1
Method	BLASTX
NCBI GI	g3355486
BLAST score	367
E value	4.0e-35
Match length	97
% identity	68
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.	235856
Seq. ID	uC-gsflmaxxa058b04b1
Method	BLASTX
NCBI GI	g2497953
BLAST score	361
E value	1.0e-34
Match length	98
% identity	73
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1). >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]
Seq. No.	235857
Seq. ID	uC-gsflmaxxa058b10b1
Method	BLASTX
NCBI GI	g4185139
BLAST score	299
E value	2.0e-27
Match length	93
% identity	62
NCBI Description	(AC005724) putative diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.	235858
Seq. ID	uC-gsflmaxxa058c02b1
Method	BLASTX
NCBI GI	g3169178
BLAST score	199
E value	2.0e-15
Match length	59
% identity	63
NCBI Description	(AC004401) hypothetical protein [Arabidopsis thaliana]
Seq. No.	235859
Seq. ID	uC-gsflmaxxa058c03b1
Method	BLASTX
NCBI GI	g2501449
BLAST score	245
E value	1.0e-20
Match length	53

to 320) [Citrullus lanatus]

Seq. No. 235865
 Seq. ID uC-gsflmaxxa058f12b1
 Method BLASTX
 NCBI GI g3822403
 BLAST score 203
 E value 8.0e-16
 Match length 40
 % identity 85
 NCBI Description (AF087932) hydroperoxide lyase [Arabidopsis thaliana]

Seq. No. 235866
 Seq. ID uC-gsflmaxxa058g07b1
 Method BLASTX
 NCBI GI g1663722
 BLAST score 386
 E value 2.0e-37
 Match length 133
 % identity 53
 NCBI Description (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 235867
 Seq. ID uC-gsflmaxxa058h08b1
 Method BLASTX
 NCBI GI g1491615
 BLAST score 261
 E value 6.0e-23
 Match length 65
 % identity 69
 NCBI Description (X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No. 235868
 Seq. ID uC-gsflmaxxa058h10b1
 Method BLASTX
 NCBI GI g2244752
 BLAST score 194
 E value 7.0e-15
 Match length 108
 % identity 39
 NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235869
 Seq. ID uC-gsflmaxxa060a04b1
 Method BLASTX
 NCBI GI g4103152
 BLAST score 165
 E value 5.0e-12
 Match length 59
 % identity 56
 NCBI Description (AF020716) histidyl-tRNA synthetase [Triticum aestivum]

Seq. No. 235870
 Seq. ID uC-gsflmaxxa060a06b1
 Method BLASTX
 NCBI GI g22166

BLAST score	514
E value	2.0e-52
Match length	118
% identity	81
NCBI Description	(X15711) adenine nucleotide translocator [Zea mays]
Seq. No.	235871
Seq. ID	uC-gsflmaxxa060b09b1
Method	BLASTX
NCBI GI	g3036816
BLAST score	204
E value	5.0e-16
Match length	131
% identity	37
NCBI Description	(AL022373) myosin-like protein [Arabidopsis thaliana]
Seq. No.	235872
Seq. ID	uC-gsflmaxxa060c12b1
Method	BLASTX
NCBI GI	g2924503
BLAST score	213
E value	3.0e-17
Match length	76
% identity	50
NCBI Description	(AL022019) glucosyltransferase [Schizosaccharomyces pombe]
Seq. No.	235873
Seq. ID	uC-gsflmaxxa060e12b1
Method	BLASTX
NCBI GI	g4309734
BLAST score	195
E value	5.0e-15
Match length	53
% identity	66
NCBI Description	(AC006439) putative 26S proteasome regulatory subunit 8 [Arabidopsis thaliana]
Seq. No.	235874
Seq. ID	uC-gsflmaxxa060f02b1
Method	BLASTX
NCBI GI	g2632252
BLAST score	345
E value	7.0e-33
Match length	88
% identity	75
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]
Seq. No.	235875
Seq. ID	uC-gsflmaxxa060f09b1
Method	BLASTX
NCBI GI	g4538913
BLAST score	317
E value	3.0e-29
Match length	97
% identity	65
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	235876
Seq. ID	uC-gsflmaxxa060f11b1
Method	BLASTX
NCBI GI	g2459415
BLAST score	146
E value	3.0e-09
Match length	83
% identity	43
NCBI Description	(AC002332) hypothetical protein [Arabidopsis thaliana]
Seq. No.	235877
Seq. ID	uC-gsflmaxxa060g02b1
Method	BLASTX
NCBI GI	g3033393
BLAST score	234
E value	1.0e-19
Match length	66
% identity	70
NCBI Description	(AC004238) putative phosphatidylinositol-glycan-class C (PIGC) [Arabidopsis thaliana]
Seq. No.	235878
Seq. ID	uC-gsflmaxxa061a02b1
Method	BLASTX
NCBI GI	g2146735
BLAST score	556
E value	2.0e-57
Match length	114
% identity	92
NCBI Description	glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone E5) - Arabidopsis thaliana (fragment) >gi_1166405_emb_CAA59011_ (X84229) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
Seq. No.	235879
Seq. ID	uC-gsflmaxxa061a09b1
Method	BLASTX
NCBI GI	g2501182
BLAST score	587
E value	7.0e-61
Match length	147
% identity	72
NCBI Description	OSMOTIN-LIKE PROTEIN PRECURSOR >gi_2129934_pir_JC5237 osmotin-like protein - tomato >gi_1220537 (L76632) osmotin-like protein [Lycopersicon esculentum]
Seq. No.	235880
Seq. ID	uC-gsflmaxxa061a11b1
Method	BLASTX
NCBI GI	g4510383
BLAST score	223
E value	3.0e-18
Match length	69
% identity	70
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.	235881

Seq. ID uC-gsflmaxxa061b01b1
 Method BLASTX
 NCBI GI g585452
 BLAST score 601
 E value 5.0e-65
 Match length 134
 % identity 90
 NCBI Description MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM
 PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)
 (NAD-ME) >gi_1076666_pir_A53318 malate dehydrogenase
 (decarboxylating) (EC 1.1.1.39) 59K chain precursor,
 mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002)
 precursor of the 59kDa subunit of the mitochondrial
 NAD+-dependent malic enzyme [Solanum tuberosum]

Seq. No. 235882
 Seq. ID uC-gsflmaxxa061b04b1
 Method BLASTX
 NCBI GI g4467110
 BLAST score 224
 E value 2.0e-18
 Match length 114
 % identity 36
 NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 235883
 Seq. ID uC-gsflmaxxa061b08b1
 Method BLASTX
 NCBI GI g2547036
 BLAST score 193
 E value 1.0e-14
 Match length 90
 % identity 53
 NCBI Description (Y13920) ribosomal protein S2 [Triticum aestivum]

Seq. No. 235884
 Seq. ID uC-gsflmaxxa061b12b1
 Method BLASTX
 NCBI GI g1495366
 BLAST score 394
 E value 3.0e-38
 Match length 104
 % identity 69
 NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 235885
 Seq. ID uC-gsflmaxxa061c06b1
 Method BLASTX
 NCBI GI g4249410
 BLAST score 148
 E value 3.0e-09
 Match length 99
 % identity 49
 NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 235886
 Seq. ID uC-gsflmaxxa061d03b1

Method BLASTX
 NCBI GI g1169451
 BLAST score 441
 E value 7.0e-44
 Match length 125
 % identity 66
 NCBI Description PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR
 ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
 (BETA-1,3-ENDOGLUCANASE) >gi_322510_pir_S31906
 beta-1,3-glucanase homolog - Arabidopsis thaliana
 >gi_22677_emb_CAA49853_(X70409) A6 [Arabidopsis thaliana]
 >gi_2244764_emb_CAB10187_(Z97335) AMP-binding protein
 [Arabidopsis thaliana]

Seq. No. 235912
 Seq. ID uC-gsflmaxxa070c06b1
 Method BLASTX
 NCBI GI g2129944
 BLAST score 331
 E value 4.0e-31
 Match length 88
 % identity 68
 NCBI Description RNA-binding protein RZ-1 - wood tobacco
 >gi_1395193_dbj_BAA12064_(D83696) RNA-binding protein RZ-1
 [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_(D28861)
 RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No. 235913
 Seq. ID uC-gsflmaxxa070c11b1
 Method BLASTX
 NCBI GI g3292827
 BLAST score 234
 E value 1.0e-19
 Match length 51
 % identity 82
 NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 235914
 Seq. ID uC-gsflmaxxa070e03b1
 Method BLASTX
 NCBI GI g3256068
 BLAST score 164
 E value 3.0e-23
 Match length 109
 % identity 50
 NCBI Description (Y14068) Heat Shock Factor 3 [Arabidopsis thaliana]

Seq. No. 235915
 Seq. ID uC-gsflmaxxa070g12b1
 Method BLASTX
 NCBI GI g3790587
 BLAST score 400
 E value 4.0e-39
 Match length 99
 % identity 73
 NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
 thaliana]

090416-101000

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Seq. No.      235930
Seq. ID       uC-gsflmaxxa076e09b1
Method        BLASTX
NCBI GI       q2642428
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Seq. No. 235936
 Seq. ID uC-gsflmaxxa088b09b1
 Method BLASTX
 NCBI GI g2244956
 BLAST score 220
 E value 5.0e-18
 Match length 133
 % identity 38
 NCBI Description (Z97340) strong similarity to pectinesterase [Arabidopsis thaliana]

Seq. No. 235937
 Seq. ID uC-gsflmaxxa088b10b1
 Method BLASTX
 NCBI GI g3367515
 BLAST score 279
 E value 8.0e-25
 Match length 97
 % identity 56
 NCBI Description (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb_AF020814 from Pisum sativum. [Arabidopsis thaliana]

Seq. No. 235938
 Seq. ID uC-gsflmaxxa088c07b1
 Method BLASTX
 NCBI GI g3928084
 BLAST score 485
 E value 7.0e-49
 Match length 148
 % identity 66
 NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No. 235939
 Seq. ID uC-gsflmaxxa088d12b1
 Method BLASTX
 NCBI GI g2832649
 BLAST score 392
 E value 7.0e-38
 Match length 95
 % identity 79
 NCBI Description (AL021710) adenylosuccinate lyase - like protein [Arabidopsis thaliana]

Seq. No. 235940
 Seq. ID uC-gsflmaxxa088e08b1
 Method BLASTX
 NCBI GI g3641252
 BLAST score 404
 E value 1.0e-39
 Match length 111
 % identity 72
 NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Match length 38
 % identity 79
 NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
 >gi_485498_pir_S33533·heat shock protein 90 homolog
 precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94
 homologue [Hordeum vulgare]

Seq. No. 235952
 Seq. ID uC-gsflmaxxa089h11b1
 Method BLASTX
 NCBI GI g2344901
 BLAST score 724
 E value 7.0e-77
 Match length 164
 % identity 82
 NCBI Description (AC002388) serine/threonine protein kinase isolog
 [Arabidopsis thaliana]

Seq. No. 235953
 Seq. ID uC-gsflmaxxa090a06b1
 Method BLASTX
 NCBI GI g2982311
 BLAST score 200
 E value 5.0e-16
 Match length 49
 % identity 78
 NCBI Description (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea
 mariana]

Seq. No. 235954
 Seq. ID uC-gsflmaxxa090c04b1
 Method BLASTX
 NCBI GI g3522942
 BLAST score 575
 E value 2.0e-59
 Match length 155
 % identity 66
 NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235955
 Seq. ID uC-gsflmaxxa090c06b1
 Method BLASTX
 NCBI GI g421955
 BLAST score 515
 E value 6.0e-59
 Match length 160
 % identity 65
 NCBI Description hypothetical protein 4 - potato transposon Tst1
 >gi_21434_emb_CAA36616_ (X52387) ORF4 [Solanum tuberosum]

Seq. No. 235956
 Seq. ID uC-gsflmaxxa090c11b1
 Method BLASTX
 NCBI GI g2529677
 BLAST score 492
 E value 6.0e-50
 Match length 115

NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235968
Seq. ID uC-gsflmaxxa091f04b1
Method BLASTX
NCBI GI g1872521
BLAST score 191
E value 2.0e-14

Match length 51
% identity 25
NCBI Description (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
>gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No. 235969
Seq. ID uC-gsflmaxxa091g01b1
Method BLASTX
NCBI GI g416664
BLAST score 388
E value 1.0e-37
Match length 113
% identity 68

NCBI Description PLASMA MEMBRANE ATPASE 4 (PROTON PUMP)
>gi_485504_pir_S33548 H⁺-transporting ATPase (EC 3.6.1.35)
type 4, plasma membrane - curled-leaved tobacco
>gi_19704_emb_CAA47275 (X66737) plasma membrane H⁺-ATPase
[Nicotiana glauca]

Seq. No. 235970
Seq. ID uC-gsflmaxxa091g03b1
Method BLASTX
NCBI GI g1621012
BLAST score 642
E value 2.0e-67
Match length 134
% identity 90

NCBI Description (Y08786) 1,4-alpha-glucan branching enzyme [Solanum tuberosum]

Seq. No. 235971
Seq. ID uC-gsflmaxxa091g05b1
Method BLASTX
NCBI GI g4454471
BLAST score 145
E value 4.0e-09
Match length 58
% identity 55

NCBI Description (AC006234) putative G protein coupled receptor [Arabidopsis thaliana]

Seq. No. 235972
Seq. ID uC-gsflmaxxa091g07b1
Method BLASTX
NCBI GI g3608485
BLAST score 439
E value 2.0e-43
Match length 87

BLAST score	312
E value	1.0e-28
Match length	69
% identity	83
NCBI Description	(L22305) corC [Medicago sativa]
Seq. No.	235999
Seq. ID	uC-gsflmaxxa096d12b1
Method	BLASTX
NCBI GI	g2558660
BLAST score	369
E value	3.0e-35
Match length	157
% identity	50
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.	236000
Seq. ID	uC-gsflmaxxa096e04b1
Method	BLASTX
NCBI GI	g3850999
BLAST score	334
E value	3.0e-31
Match length	91
% identity	75
NCBI Description	(AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1 [Zea mays]
Seq. No.	236001
Seq. ID	uC-gsflmaxxa096e07b1
Method	BLASTX
NCBI GI	g2760839
BLAST score	226
E value	1.0e-18
Match length	73
% identity	55
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]
Seq. No.	236002
Seq. ID	uC-gsflmaxxa096e11b1
Method	BLASTX
NCBI GI	g4567249
BLAST score	499
E value	2.0e-50
Match length	133
% identity	68
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.	236003
Seq. ID	uC-gsflmaxxa096g10b1
Method	BLASTX
NCBI GI	g2388580
BLAST score	753
E value	3.0e-80
Match length	155
% identity	89
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (qb 1253956). [Arabidopsis thaliana]


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Seq. No.      236004
Seq. ID      uC-gsflmaxxa096h01b1
Method      BLASTX
NCBI GI      g2244799
BLAST score   196
E value      3.0e-15
Match length  98
% identity    46
NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
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Seq. No.          236005
Seq. ID           uC-gsflmaxxa096h04b1
Method            BLASTX
NCBI GI           g1483177
BLAST score       324
E value           6.0e-30
Match length      141
% identity        45
NCBI Description   (D86598) antifreeze-like protein (af70) [Picea abies]
```

```
Seq. No.      236006
Seq. ID      uC-gsflmaxxa097b10b1
Method       BLASTX
NCBI GI      g4063751
BLAST score   323
E value      6.0e-30
Match length  138
% identity    54
NCBI Description
              (AC005851) putative white protein [Arabidopsis thaliana]
              >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
              protein [Arabidopsis thaliana]
```

Seq. No.	236007
Seq. ID	uC-gsflmaxxa097b12b1
Method	BLASTX
NCBI GI	g2708745
BLAST score	544
E value	6.0e-56
Match length	120
% identity	86
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

```
Seq. No.      236008
Seq. ID      uC-gsflmaxxa097c11b1
Method       BLASTX
NCBI GI      g1707032
BLAST score   148
E value      1.0e-09
Match length  83
% identity    43
NCBI Description (U80445) coded for by C. elegans cDNA yk13g5.3; coded for
by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA
CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for
by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA
yk65h8
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Seq. No.      236015
Seq. ID       uC-gsflmaxxa097h06b1
Method        BLASTX
NCBI GI       g3228517
BLAST score   429
E value       2.0e-42
Match length  133
% identity    63
NCBI Description (AF007788) ETTIN [Arabidopsis thaliana]
```

```
Seq. No.      236016
Seq. ID      uC-gsflmaxxa097h10b1
Method       BLASTX
NCBI GI      g3850816
BLAST score   454
E value      2.0e-45
Match length  86
% identity    93
NCBI Description (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
satival]
```

```
Seq. No.      236017
Seq. ID      uC-gsflmaxxa098b02b1
Method       BLASTX
NCBI GI      g3763917
BLAST score   452
E value      6.0e-45
Match length  129
% identity    71
NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]
               >gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224)
               hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      236018
Seq. ID       uC-gsflmaxxa098b06b1
Method        BLASTX
NCBI GI       g1705491
BLAST score    144
E value        6.0e-09
Match length   119
% identity     33
NCBI Description (U50068) C01G5.8 gene product [Caenorhabditis elegans]
```


Seq. No.	236019
Seq. ID	uC-gsflmaxxa098b11b1
Method	BLASTX
NCBI GI	g82306
BLAST score	605
E value	7.0e-63
Match length	127
% identity	87
NCBI Description	myb protein 305 - garden snapdragon
Seq. No.	236020
Seq. ID	uC-gsflmaxxa098b12b1
Method	BLASTX
NCBI GI	g4538926
BLAST score	276
E value	2.0e-24
Match length	94
% identity	56
NCBI Description	(AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]
Seq. No.	236021
Seq. ID	uC-gsflmaxxa098c07b1
Method	BLASTX
NCBI GI	g2511693
BLAST score	270
E value	1.0e-23
Match length	71
% identity	73
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.	236022
Seq. ID	uC-gsflmaxxa098c11b1
Method	BLASTX
NCBI GI	g120672
BLAST score	722
E value	1.0e-76
Match length	162
% identity	87
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66016_pir_DEPZG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - parsley >gi_20549_emb_CAA42902_(X60344) glyceraldehyde 3-phosphate dehydrogenase [Petroselinum crispum]
Seq. No.	236023
Seq. ID	uC-gsflmaxxa098d04b1
Method	BLASTX
NCBI GI	g1168537
BLAST score	338
E value	1.0e-31
Match length	132
% identity	51
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir_JS0732 aspartic proteinase (EC 3.4.23.-) - rice >gi_218143_dbj_BAA02242_(D12777) aspartic proteinase

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Seq. No.      236029
Seq. ID       uC-gsflmaxxa098h11b1
Method        BLASTX
NCBI GI       q2342684
```


BLAST score	260
E value	1.0e-22
Match length	118
% identity	47
NCBI Description	(AC000106) F7G19.14 [Arabidopsis thaliana]
Seq. No.	236030
Seq. ID	uC-gsflmaxxa098h12b1
Method	BLASTX
NCBI GI	g2507229
BLAST score	518
E value	9.0e-53
Match length	133
% identity	74
NCBI Description	40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN) >gi_423247_pir_A46579 estrogen receptor-binding cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074) cyclophilin [Bos taurus]
Seq. No.	236031
Seq. ID	uC-gsflmaxxa106c02b1
Method	BLASTX
NCBI GI	g4325341
BLAST score	216
E value	9.0e-18
Match length	53
% identity	79
NCBI Description	(AF128393) similar to the Drosophila DES-1 protein (GB:X94180) [Arabidopsis thaliana]
Seq. No.	236032
Seq. ID	uC-gsflmaxxa107a01b1
Method	BLASTX
NCBI GI	g4049341
BLAST score	386
E value	2.0e-37
Match length	87
% identity	89
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]
Seq. No.	236033
Seq. ID	uC-gsflmaxxa107a07b1
Method	BLASTX
NCBI GI	g3335375
BLAST score	278
E value	3.0e-25
Match length	61
% identity	85
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]
Seq. No.	236034
Seq. ID	uC-gsflmaxxa107b12b1
Method	BLASTX
NCBI GI	g3694872
BLAST score	394

Match length	93
% identity	39
NCBI Description	(U89793) allergen Amb a VI [Ambrosia artemisiifolia]
Seq. No.	236040
Seq. ID	uC-gsflmaxxa119c02b1
Method	BLASTX
NCBI GI	g1076511
BLAST score	145
E value	1.0e-09
Match length	31
% identity	90
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]
Seq. No.	236041
Seq. ID	uC-gsflmaxxa119c07b1
Method	BLASTX
NCBI GI	g1916292
BLAST score	157
E value	1.0e-10
Match length	65
% identity	42
NCBI Description	(U89793) allergen Amb a VI [Ambrosia artemisiifolia]
Seq. No.	236042
Seq. ID	uC-gsflnu33B001a01b1
Method	BLASTX
NCBI GI	g2244898
BLAST score	364
E value	1.0e-34
Match length	150
% identity	46
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.	236043
Seq. ID	uC-gsflnu33B001b03b1
Method	BLASTX
NCBI GI	g2739168
BLAST score	179
E value	6.0e-16
Match length	87
% identity	56
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]
Seq. No.	236044
Seq. ID	uC-gsflnu33B001b05b1
Method	BLASTX
NCBI GI	g1330401
BLAST score	133
E value	1.0e-08
Match length	76
% identity	46
NCBI Description	(U58762) T27F7.1 gene product [Caenorhabditis elegans]

Seq. No. 236045
 Seq. ID uC-gsflnu33B001b09b1
 Method BLASTX
 NCBI GI g3600052
 BLAST score 275
 E value 2.0e-24
 Match length 94
 % identity 56
 NCBI Description (AF080120) contains similarity to glycosyl hydrolases family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03) [Arabidopsis thaliana]

Seq. No. 236046
 Seq. ID uC-gsflnu33B001b11b1
 Method BLASTX
 NCBI GI g4322421
 BLAST score 233
 E value 2.0e-19
 Match length 133
 % identity 41
 NCBI Description (AF085230) cadmium resistance factor 1 [Arabidopsis thaliana]

Seq. No. 236047
 Seq. ID uC-gsflnu33B001c09b1
 Method BLASTX
 NCBI GI g1184075
 BLAST score 153
 E value 5.0e-10
 Match length 140
 % identity 3
 NCBI Description (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon esculentum]

Seq. No. 236048
 Seq. ID uC-gsflnu33B001d05b1
 Method BLASTX
 NCBI GI g2982268
 BLAST score 472
 E value 2.0e-47
 Match length 93
 % identity 98
 NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No. 236049
 Seq. ID uC-gsflnu33B001e09b1
 Method BLASTX
 NCBI GI g1816459
 BLAST score 531
 E value 3.0e-54
 Match length 133
 % identity 80
 NCBI Description (Y10750) DEFH125 protein [Antirrhinum majus]

BLAST score 236
 E value 5.0e-34
 Match length 93
 % identity 82
 NCBI Description SYNTAXIN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451)
 syntaxin-related [Arabidopsis thaliana] >gi_1184167
 (U39452) syntaxin-related [Arabidopsis thaliana]
 >gi_3063443 (AC003981) F22013.4 [Arabidopsis thaliana]
 >gi_1587182_prf_2206310A syntaxin-related protein
 [Arabidopsis thaliana]

Seq. No. 236056
 Seq. ID uC-gsflnu33B002f12b1
 Method BLASTX
 NCBI GI g4469025
 BLAST score 179
 E value 1.0e-13
 Match length 61
 % identity 37
 NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 236057
 Seq. ID uC-gsflnu33B003a02b1
 Method BLASTX
 NCBI GI g4220480
 BLAST score 167
 E value 1.0e-11
 Match length 97
 % identity 36
 NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 236058
 Seq. ID uC-gsflnu33B003a09b1
 Method BLASTX
 NCBI GI g2440044
 BLAST score 533
 E value 1.0e-54
 Match length 111
 % identity 89
 NCBI Description (AJ001293) major intrinsic protein PIPB [Craterostigma
 plantagineum]

Seq. No. 236059
 Seq. ID uC-gsflnu33B003b06b1
 Method BLASTX
 NCBI GI g3172025
 BLAST score 364
 E value 6.0e-35
 Match length 106
 % identity 67
 NCBI Description (AB005805) aldehyde oxidase [Arabidopsis thaliana]

Seq. No. 236060
 Seq. ID uC-gsflnu33B003d04b1
 Method BLASTX
 NCBI GI g2960358
 BLAST score 209

BLAST score 417
 E value 6.0e-41
 Match length 89
 % identity 88
 NCBI Description (AC000106) Similar to Schizosaccharomyces CCAAT-binding factor (gb_U88525). EST gb_T04310 comes from this gene. [Arabidopsis thaliana]

Seq. No. 236071
 Seq. ID uC-gsflnu33B004h06b1
 Method BLASTX
 NCBI GI g2689720
 BLAST score 432
 E value 2.0e-57
 Match length 159
 % identity 73
 NCBI Description (AF037168) DnaJ homologue [Arabidopsis thaliana]

Seq. No. 236072
 Seq. ID uC-gsflnu33B005b12b1
 Method BLASTX
 NCBI GI g2245061
 BLAST score 307
 E value 4.0e-28
 Match length 68
 % identity 87
 NCBI Description (Z97342) Clp proteinase homolog [Arabidopsis thaliana]

Seq. No. 236073
 Seq. ID uC-gsflnu33B005d02b1
 Method BLASTX
 NCBI GI g3757521
 BLAST score 470
 E value 3.0e-47
 Match length 132
 % identity 64
 NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 236074
 Seq. ID uC-gsflnu33B005d03b1
 Method BLASTX
 NCBI GI g1703446
 BLAST score 497
 E value 2.0e-50
 Match length 130
 % identity 78
 NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
 >gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
 >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No. 236075
 Seq. ID uC-gsflnu33B005d08b1
 Method BLASTX
 NCBI GI g3894393
 BLAST score 185
 E value 7.0e-14

Seq. ID	uC-gsflnu33B006c02b1
Method	BLASTX
NCBI GI	g2961343
BLAST score	201
E value	1.0e-15
Match length	40
% identity	95
NCBI Description	(AL022140) symbiosis-related like protein [Arabidopsis thaliana]
Seq. No.	236087
Seq. ID	uC-gsflnu33B006d02b1
Method	BLASTX
NCBI GI	g4490305
BLAST score	407
E value	9.0e-40
Match length	147
% identity	54
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]
Seq. No.	236088
Seq. ID	uC-gsflnu33B006f04b1
Method	BLASTX
NCBI GI	g120669
BLAST score	252
E value	8.0e-22
Match length	59
% identity	78
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_(X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.	236089
Seq. ID	uC-gsflnu33B006f06b1
Method	BLASTX
NCBI GI	g1076257
BLAST score	178
E value	1.0e-13
Match length	31
% identity	97
NCBI Description	sucrose-proton symporter - beet >gi_633172_emb_CAA58730_(X83850) sucrose/proton-symporter [Beta vulgaris]
Seq. No.	236090
Seq. ID	uC-gsflnu33B006g07b1
Method	BLASTX
NCBI GI	g2961390
BLAST score	347
E value	7.0e-33
Match length	84
% identity	74
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]
Seq. No.	236091

Seq. ID uC-gsflnu33B006g12b1
 Method BLASTX
 NCBI GI g4115937
 BLAST score 301
 E value 7.0e-39
 Match length 101
 % identity 75
 NCBI Description (AF118223) contains similarity to human PCF11p homolog
 (GB:AF046935) [Arabidopsis thaliana]

Seq. No. 236092
 Seq. ID uC-gsflnu33B006h10b1
 Method BLASTX
 NCBI GI g2983537
 BLAST score 147
 E value 2.0e-09
 Match length 55
 % identity 53
 NCBI Description (AE000720) phosphate transport ATP binding protein [Aquifex
 aeolicus]

Seq. No. 236093
 Seq. ID uC-gsflnu33B006h11b1
 Method BLASTX
 NCBI GI g2583112
 BLAST score 153
 E value 1.0e-10
 Match length 42
 % identity 67
 NCBI Description (AC002387) putative PD1-like DNA-binding protein
 [Arabidopsis thaliana]

Seq. No. 236094
 Seq. ID uC-gsflnu33B008a04b1
 Method BLASTX
 NCBI GI g4539401
 BLAST score 289
 E value 7.0e-26
 Match length 109
 % identity 61
 NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

Seq. No. 236095
 Seq. ID uC-gsflnu33B008b01b1
 Method BLASTX
 NCBI GI g1706794
 BLAST score 361
 E value 3.0e-34
 Match length 121
 % identity 55
 NCBI Description BIS(5'-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE
 5',5'''-P1,P3-TRIPHOSPHATE HYDROLASE)
 (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE)
 (FRAGILE HISTIDINE TRIAD PROTEIN) >gi_3114520_pdb_4FIT_
 Fhit-Apo >gi_3114524_pdb_6FIT_ Fhit-Transition State
 Analog >gi_3318895_pdb_1FHI_ Substrate Analog (Ib2)
 Complex With The Fragile Histidine Triad Protein, Fhit

09634016 = 101000

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Seq. No.      236097
Seq. ID       uC-gsflnu33B008b12b1
Method        BLASTX
NCBI GI       g1914685
BLAST score    283
E value        2.0e-25
Match length   113
% identity     54
NCBI Description (Y12014) RAD23 protein, isoform II [Daucus carota]
```

```
Seq. No.      236099
Seq. ID       uC-gsflnu33B008c10b1
Method        BLASTX
NCBI GI       g4539373
BLAST score   142
E value       7.0e-09
Match length  84
% identity    38
NCBI Description (AL049525) putative retrotransposon polyprotein
                [Arabidopsis thaliana]
```

34211

% identity 90
 NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 236101
 Seq. ID uC-gsflnu33B008e09b1
 Method BLASTX
 NCBI GI g2982309
 BLAST score 167
 E value 1.0e-23
 Match length 98
 % identity 50
 NCBI Description (AF051239) probable ubiquitin activating enzyme 2 [Picea mariana]

Seq. No. 236102
 Seq. ID uC-gsflnu33B008f06b1
 Method BLASTX
 NCBI GI g3420239
 BLAST score 261
 E value 3.0e-23
 Match length 49
 % identity 100
 NCBI Description (AF059484) actin [Gossypium hirsutum]

Seq. No. 236103
 Seq. ID uC-gsflnu33B008f12b1
 Method BLASTX
 NCBI GI g1174448
 BLAST score 162
 E value 4.0e-11
 Match length 75
 % identity 49
 NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No. 236104
 Seq. ID uC-gsflnu33B008g12b1
 Method BLASTX
 NCBI GI g4185143
 BLAST score 246
 E value 3.0e-21
 Match length 72
 % identity 64
 NCBI Description (AC005724) putative signal recognition particle receptor beta subunit [Arabidopsis thaliana]

Seq. No. 236105
 Seq. ID uC-gsflnu33B008h05b1
 Method BLASTX
 NCBI GI g967125
 BLAST score 444
 E value 2.0e-44
 Match length 91
 % identity 95
 NCBI Description (U08140) calcium dependent protein kinase [Vigna radiata]

Method BLASTX
 NCBI GI g3335359
 BLAST score 488
 E value 3.0e-49
 Match length 106
 % identity 87
 NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 236112
 Seq. ID uC-gsflnu33B009h11b1
 Method BLASTX
 NCBI GI g4432840
 BLAST score 173
 E value 2.0e-12
 Match length 95
 % identity 42
 NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 236113
 Seq. ID uC-gsflnu33B011a02b1
 Method BLASTX
 NCBI GI g3080417
 BLAST score 346
 E value 9.0e-33
 Match length 89
 % identity 83
 NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 236114
 Seq. ID uC-gsflnu33B011b05b1
 Method BLASTX
 NCBI GI g2529670
 BLAST score 236
 E value 8.0e-20
 Match length 79
 % identity 61
 NCBI Description (AC002535) ribosomal protein L18-like [Arabidopsis thaliana]

Seq. No. 236115
 Seq. ID uC-gsflnu33B011d04b1
 Method BLASTX
 NCBI GI g3220021
 BLAST score 224
 E value 3.0e-23
 Match length 125
 % identity 46
 NCBI Description (U57828) lipase homolog [Arabidopsis thaliana]

Seq. No. 236116
 Seq. ID uC-gsflnu33B011d07b1
 Method BLASTX
 NCBI GI g4105633
 BLAST score 204
 E value 6.0e-16
 Match length 56
 % identity 71

Method BLASTX
 NCBI GI g1717744
 BLAST score 222
 E value 5.0e-18
 Match length 108
 % identity 42
 NCBI Description TOPOISOMERASE 1-RELATED PROTEIN TRF4
 >gi_1077298_pir_S51882 topoisomerase I-related protein
 TRF4 - yeast (*Saccharomyces cerevisiae*)
 >gi_663237_emb_CAA88145_(Z48149) ORF [*Saccharomyces*
cerevisiae] >gi_950226 (U31355) Trf4p [*Saccharomyces*
cerevisiae] >gi_1419987_emb_CAA99134_(Z74857) ORF YOL115w
 [*Saccharomyces cerevisiae*]

Seq. No. 236123
 Seq. ID uC-gsflnu33B011g09b1
 Method BLASTX
 NCBI GI g2213600
 BLAST score 161
 E value 2.0e-11
 Match length 80
 % identity 46
 NCBI Description (AC000348) T7N9.20 [*Arabidopsis thaliana*]

Seq. No. 236124
 Seq. ID uC-gsflnu33B011h06b1
 Method BLASTX
 NCBI GI g3953470
 BLAST score 149
 E value 1.0e-09
 Match length 80
 % identity 49
 NCBI Description (AC002328) F20N2.15 [*Arabidopsis thaliana*]

Seq. No. 236125
 Seq. ID uC-gsflnu33B012c08b1
 Method BLASTX
 NCBI GI g3832528
 BLAST score 524
 E value 1.0e-53
 Match length 126
 % identity 81
 NCBI Description (AF100167) unknown [*Glycine max*]

Seq. No. 236126
 Seq. ID uC-gsflnu33B012d01b1
 Method BLASTX
 NCBI GI g3287693
 BLAST score 434
 E value 5.0e-43
 Match length 90
 % identity 89
 NCBI Description (AC003979) Similar to LIM17 gene product gb_1653769 from
 the genome of *Synechocystis* sp. gb_D90916. [*Arabidopsis*
thaliana]

Seq. No. 236127

Seq. ID uC-gsflnu33B012e08b1
 Method BLASTX
 NCBI GI g2062170
 BLAST score 272
 E value 5.0e-24
 Match length 136
 % identity 52
 NCBI Description (AC001645) unknown protein [Arabidopsis thaliana]

Seq. No. 236128
 Seq. ID uC-gsflnu33B012g08b1
 Method BLASTX
 NCBI GI g2244847
 BLAST score 246
 E value 5.0e-21
 Match length 105
 % identity 54
 NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No. 236129
 Seq. ID uC-gsflnu33B013a03b1
 Method BLASTX
 NCBI GI g3647283
 BLAST score 554
 E value 5.0e-57
 Match length 144
 % identity 74
 NCBI Description (AJ011418) ubiquitin activating enzyme [Lycopersicon esculentum]

Seq. No. 236130
 Seq. ID uC-gsflnu33B013a06b1
 Method BLASTX
 NCBI GI g1587206
 BLAST score 363
 E value 8.0e-56
 Match length 148
 % identity 80
 NCBI Description T complex protein [Cucumis sativus]

Seq. No. 236131
 Seq. ID uC-gsflnu33B013a07b1
 Method BLASTX
 NCBI GI g4115377
 BLAST score 196
 E value 4.0e-15
 Match length 94
 % identity 43
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 236132
 Seq. ID uC-gsflnu33B013a10b1
 Method BLASTX
 NCBI GI g2213626
 BLAST score 239
 E value 5.0e-20

Match length 120
 % identity 42
 NCBI Description (AC000103) F21J9.18 [Arabidopsis thaliana]

Seq. No. 236133
 Seq. ID uC-gsflnu33B013b10b1
 Method BLASTX
 NCBI GI g2244759
 BLAST score 542
 E value 1.0e-55
 Match length 137
 % identity 72
 NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No. 236134
 Seq. ID uC-gsflnu33B013b11b1
 Method BLASTX
 NCBI GI g3928084
 BLAST score 515
 E value 2.0e-52
 Match length 152
 % identity 64
 NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No. 236135
 Seq. ID uC-gsflnu33B013f11b1
 Method BLASTX
 NCBI GI g1352186
 BLAST score 523
 E value 3.0e-53
 Match length 123
 % identity 77
 NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No. 236136
 Seq. ID uC-gsflnu33B013f12b1
 Method BLASTX
 NCBI GI g4567262
 BLAST score 520
 E value 6.0e-63
 Match length 132
 % identity 89
 NCBI Description (AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No. 236137
 Seq. ID uC-gsflnu33B015a03b1
 Method BLASTX
 NCBI GI g4455340
 BLAST score 466
 E value 1.0e-46
 Match length 131
 % identity 66
 NCBI Description (AL035522) putative protein [Arabidopsis thaliana]

Seq. No. 236138
 Seq. ID uC-gsflnu33B015a04b1
 Method BLASTX
 NCBI GI g1723894
 BLAST score 272
 E value 7.0e-24
 Match length 164
 % identity 40
 NCBI Description HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC
 REGION >gi_2131584_pir_S64106 hypothetical protein YGL099w
 - yeast (*Saccharomyces cerevisiae*)
 >gi_1322637_emb_CAA96805_ (Z72621) ORF YGL099w
 [*Saccharomyces cerevisiae*]

Seq. No. 236139
 Seq. ID uC-gsflnu33B015a09b1
 Method BLASTX
 NCBI GI g464707
 BLAST score 571
 E value 4.0e-59
 Match length 117
 % identity 95
 NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal
 protein S18.A - *Arabidopsis thaliana*
 >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
 [*Arabidopsis thaliana*] >gi_434343_emb_CAA82273_ (Z28701)
 S18 ribosomal protein [*Arabidopsis thaliana*]
 >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
 [*Arabidopsis thaliana*] >gi_434906_emb_CAA82275_ (Z28962)
 S18 ribosomal protein [*Arabidopsis thaliana*]
 >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
 [*Arabidopsis thaliana*] >gi_3287678 (AC003979) Match to
 ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
 thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
 gb_R30430 come from this gene. [*Arabidopsis thaliana*]
 >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
 protein [*Arabidopsis thaliana*]

Seq. No. 236140
 Seq. ID uC-gsflnu33B015b01b1
 Method BLASTX
 NCBI GI g3334157
 BLAST score 516
 E value 4.0e-70
 Match length 155
 % identity 82
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
 (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
 >gi_1220142_emb_CAA59468_ (X85185) cyclophilin
 [*Catharanthus roseus*]

Seq. No. 236141
 Seq. ID uC-gsflnu33B015b09b1
 Method BLASTX
 NCBI GI g4376203
 BLAST score 343
 E value 3.0e-32

quaking aspen >gi_20951_emb_CAA44006_ (X62096) lignin
bispecific acid/5-hydroxyferulic acid methyltransferase
[Populus tremuloides] >gi_2226267 (U13171) caffeic
acid/5-hydroxyferulic acid O-methyltransferase [Populus
tremuloides]

Seq. No. 236152
Seq. ID uC-gsflnu33B016c08b1
Method BLASTX
NCBI GI g1173043
BLAST score 259
E value 2.0e-22
Match length 69
% identity 77
NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi_479441_pir_S33899 ribosomal
protein L38 - tomato (cv. Moneymaker)
>gi_313027_emb_CAA49599_ (X69979) ribosomal protein L38
[Lycopersicon esculentum]

Seq. No. 236153
Seq. ID uC-gsflnu33B016c12b1
Method BLASTX
NCBI GI g401189
BLAST score 146
E value 1.0e-09
Match length 40
% identity 78
NCBI Description WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP)
(TURGOR-RESPONSIVE PROTEIN 7A) >gi_485511_pir_S33617
trg-31 protein - garden pea >gi_20426_emb_CAA79159_
(Z18288) trg-31 [Pisum sativum]

Seq. No. 236154
Seq. ID uC-gsflnu33B016d11b1
Method BLASTX
NCBI GI g2462834
BLAST score 325
E value 4.0e-30
Match length 151
% identity 42
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236155
Seq. ID uC-gsflnu33B016e04b1
Method BLASTX
NCBI GI g3941480
BLAST score 356
E value 1.0e-33
Match length 164
% identity 48
NCBI Description (AF062894) putative transcription factor [Arabidopsis
thaliana]

Seq. No. 236156
Seq. ID uC-gsflnu33B016f11b1
Method BLASTX
NCBI GI g3377822

BLAST score 314
 E value 6.0e-29
 Match length 76
 % identity 83
 NCBI Description (AF076275) contains similarity to *Caenorhabditis elegans* MEL-26 (GB:U67737) [*Arabidopsis thaliana*]

Seq. No. 236157
 Seq. ID uC-gsflnu33B016f12b1
 Method BLASTX
 NCBI GI g2809246
 BLAST score 347
 E value 8.0e-33
 Match length 123
 % identity 59
 NCBI Description (AC002560) F2401.15 [*Arabidopsis thaliana*]

Seq. No. 236158
 Seq. ID uC-gsflnu33B016g05b1
 Method BLASTX
 NCBI GI g1480012
 BLAST score 157
 E value 7.0e-11
 Match length 30
 % identity 93
 NCBI Description (D78492) putative ubiquitin extension protein [*Brassica rapa*]

Seq. No. 236159
 Seq. ID uC-gsflnu33B016g06b1
 Method BLASTX
 NCBI GI g585628
 BLAST score 164
 E value 2.0e-11
 Match length 40
 % identity 78
 NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-1 CATALYTIC SUBUNIT >gi_418779_pir_S31162 phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain (clone EP14a) - *Arabidopsis thaliana* >gi_166823 (M96733) protein phosphatase [*Arabidopsis thaliana*]

Seq. No. 236160
 Seq. ID uC-gsflnu33B016g09b1
 Method BLASTX
 NCBI GI g132935
 BLAST score 214
 E value 2.0e-17
 Match length 65
 % identity 60
 NCBI Description 60S RIBOSOMAL PROTEIN L37A (YL37) (RP47)
 >gi_101568_pir_S18431 ribosomal protein L35a.e.c16 - yeast (*Saccharomyces cerevisiae*) >gi_4392_emb_CAA41035 (X57969) ribosomal protein L37a [*Saccharomyces cerevisiae*]
 >gi_1244773 (U43703) Lpi4p [*Saccharomyces cerevisiae*]
 >gi_1370305_emb_CAA97847 (Z73499) ORF YPL143w [*Saccharomyces cerevisiae*]

cv. Alexis, aleurone, Peptide, 516 aa]
 >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3
 [Hordeum vulgare]

Seq. No. 236177
 Seq. ID uC-gsflnu33B018h08b1
 Method BLASTX
 NCBI GI g4417304
 BLAST score 379
 E value 1.0e-36
 Match length 100
 % identity 63
 NCBI Description (AC006446) putative beta-1,4-mannosyl-glycoprotein
 beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
 thaliana]

Seq. No. 236178
 Seq. ID uC-gsflnu33B019a02b1
 Method BLASTX
 NCBI GI g3776084
 BLAST score 223
 E value 4.0e-18
 Match length 83
 % identity 48
 NCBI Description (Y18251) NtN2 [Medicago truncatula]

Seq. No. 236179
 Seq. ID uC-gsflnu33B019b01b1
 Method BLASTX
 NCBI GI g4558673
 BLAST score 311
 E value 1.0e-28
 Match length 134
 % identity 37
 NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236180
 Seq. ID uC-gsflnu33B019b10b1
 Method BLASTX
 NCBI GI g3004565
 BLAST score 259
 E value 1.0e-22
 Match length 94
 % identity 23
 NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 236181
 Seq. ID uC-gsflnu33B019c05b1
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 9.0e-15
 Match length 47
 % identity 68
 NCBI Description (AF116845) metallothionein-like type 1 protein. [Ipomoea
 batatas]

NCBI GI g3367523
 BLAST score 185
 E value 1.0e-23
 Match length 74
 % identity 69
 NCBI Description (AC004392) ESTs gb_AA728658 and gb_N95943 come from this gene. [Arabidopsis thaliana]

Seq. No. 236188
 Seq. ID uC-gsflnu33B019h06b1
 Method BLASTX
 NCBI GI g2980641
 BLAST score 194
 E value 3.0e-20
 Match length 89
 % identity 44
 NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No. 236189
 Seq. ID uC-gsflnu33B019h09b1
 Method BLASTX
 NCBI GI g2213610
 BLAST score 377
 E value 3.0e-36
 Match length 105
 % identity 27
 NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No. 236190
 Seq. ID uC-gsflnu33B019h12b1
 Method BLASTX
 NCBI GI g2623309
 BLAST score 313
 E value 8.0e-29
 Match length 130
 % identity 52
 NCBI Description (AC002409) similar to tgacg-specific DNA-binding protein [Arabidopsis thaliana]

Seq. No. 236191
 Seq. ID uC-gsflnu33B022a12b1
 Method BLASTX
 NCBI GI g4204259
 BLAST score 333
 E value 4.0e-31
 Match length 108
 % identity 68
 NCBI Description (AC005223) 18074 [Arabidopsis thaliana]

Seq. No. 236192
 Seq. ID uC-gsflnu33B022b03b1
 Method BLASTX
 NCBI GI g4539660
 BLAST score 388
 E value 1.0e-37
 Match length 107
 % identity 66

NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 236193
Seq. ID uC-gsflnu33B022b06b1
Method BLASTX
NCBI GI g3880625
BLAST score 248
E value 4.0e-21
Match length 82
% identity 54
NCBI Description (Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge

Seq. No. 236194
Seq. ID uC-gsflnu33B022f07b1
Method BLASTX
NCBI GI g2262099
BLAST score 466
E value 7.0e-47
Match length 99
% identity 79
NCBI Description (AC002343) thaumatin isolog [Arabidopsis thaliana]

Seq. No. 236195
Seq. ID uC-gsflnu33B022g04b1
Method BLASTX
NCBI GI g2507442
BLAST score 147
E value 2.0e-09
Match length 29
% identity 93
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1419685_emb_CAA67207_ (X98618) TCTP-like protein [Medicago sativa]

Seq. No. 236196
Seq. ID uC-gsflnu33B023a10b1
Method BLASTX
NCBI GI g913227
BLAST score 209
E value 3.0e-17
Match length 59
% identity 68
NCBI Description transcription factor X1DP-1 [Xenopus laevis, embryos, Peptide, 409 aa]

Seq. No. 236197
Seq. ID uC-gsflnu33B023a11b1
Method BLASTX
NCBI GI g3892047
BLAST score 158
E value 1.0e-10
Match length 107
% identity 37

NCBI Description (AC002330) putative bZIP-like DNA binding protein
[Arabidopsis thaliana]

Seq. No. 236198
Seq. ID uC-gsflnu33B023d05b1
Method BLASTX
NCBI GI g1296816
BLAST score 377
E value 3.0e-36
Match length 88
% identity 84
NCBI Description (X94995) naringenin-chalcone synthase [Juglans sp.]

Seq. No. 236199
Seq. ID uC-gsflnu33B023f01b1
Method BLASTX
NCBI GI g1076620
BLAST score 334
E value 2.0e-31
Match length 92
% identity 67
NCBI Description cyclin - common tobacco >gi_599933_emb_CAA86032_ (Z37978)
Cyclin [Nicotiana tabacum]

Seq. No. 236200
Seq. ID uC-gsflnu33B023f04b1
Method BLASTX
NCBI GI g2462925
BLAST score 138
E value 1.0e-08
Match length 33
% identity 82
NCBI Description (AJ000053) GTP cyclohydrolase II /
3,4-dihydroxy-2-butanone-4-phosphate synthase [Arabidopsis
thaliana]

Seq. No. 236201
Seq. ID uC-gsflnu33B023f12b1
Method BLASTX
NCBI GI g1532167
BLAST score 147
E value 2.0e-09
Match length 48
% identity 52
NCBI Description (U63815) localized according to blastn similarity to EST
sequences; therefore, the coding span corresponds only to
an area of similarity since the initiation codon and stop
codon could not be precisely determined [Arabidopsis
thaliana]

Seq. No. 236202
Seq. ID uC-gsflnu33B023g01b1
Method BLASTX
NCBI GI g4154352
BLAST score 174
E value 1.0e-12
Match length 91

Seq. No. 236208
 Seq. ID uC-gsflnu33B025b11b1
 Method BLASTX
 NCBI GI g3169719
 BLAST score 355
 E value 3.0e-34
 Match length 77
 % identity 88
 NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]

Seq. No. 236209
 Seq. ID uC-gsflnu33B025g07b1
 Method BLASTX
 NCBI GI g401189
 BLAST score 281
 E value 1.0e-25
 Match length 59
 % identity 88
 NCBI Description WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP) (TURGOR-RESPONSIVE PROTEIN 7A) >gi_485511_pir_S33617 trg-31 protein - garden pea >gi_20426_emb_CAA79159_ (Z18288) trg-31 [Pisum sativum]

Seq. No. 236210
 Seq. ID uC-gsflnu33B025g11b1
 Method BLASTX
 NCBI GI g633110
 BLAST score 157
 E value 5.0e-11
 Match length 34
 % identity 100
 NCBI Description (D31843) plasma membrane H⁺-ATPase [Oryza sativa]

Seq. No. 236211
 Seq. ID uC-gsflnu33B026a02b1
 Method BLASTX
 NCBI GI g4406819
 BLAST score 193
 E value 1.0e-14
 Match length 81
 % identity 51
 NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 236212
 Seq. ID uC-gsflnu33B026b10b1
 Method BLASTX
 NCBI GI g3005576
 BLAST score 642
 E value 2.0e-67
 Match length 134
 % identity 53
 NCBI Description (AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]

Seq. No. 236213
 Seq. ID uC-gsflnu33B026d04b1

Method	BLASTX
NCBI GI	g2739374
BLAST score	288
E value	9.0e-26
Match length	139
% identity	17
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.	236214
Seq. ID	uC-gsflnu33B026e01b1
Method	BLASTX
NCBI GI	g3080415
BLAST score	648
E value	5.0e-68
Match length	158
% identity	72
NCBI Description	(AL022604) cysteine proteinase - like protein [Arabidopsis thaliana]
Seq. No.	236215
Seq. ID	uC-gsflnu33B026e08b1
Method	BLASTX
NCBI GI	g1502430
BLAST score	505
E value	3.0e-63
Match length	145
% identity	82
NCBI Description	(U62331) phosphate transporter [Arabidopsis thaliana] >gi_2564661 (AF022872) phosphate transporter [Arabidopsis thaliana] >gi_3869206_dbj_BAA34398 (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770) phosphate transporter, AtPT2 [Arabidopsis thaliana]
Seq. No.	236216
Seq. ID	uC-gsflnu33B026e10b1
Method	BLASTX
NCBI GI	g3702327
BLAST score	272
E value	5.0e-24
Match length	104
% identity	52
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	236217
Seq. ID	uC-gsflnu33B026f04b1
Method	BLASTX
NCBI GI	g3193284
BLAST score	277
E value	1.0e-24
Match length	141
% identity	44
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]
Seq. No.	236218
Seq. ID	uC-gsflnu33B026h07b1
Method	BLASTX
NCBI GI	g2894596

BLAST score 502
 E value 6.0e-51
 Match length 130
 % identity 75
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 236219
 Seq. ID uC-gsflnu33B026h10b1
 Method BLASTX
 NCBI GI g4101564
 BLAST score 244
 E value 1.0e-20
 Match length 122
 % identity 46
 NCBI Description (AF004556) IFA-binding protein [Arabidopsis thaliana]

Seq. No. 236220
 Seq. ID uC-gsflnu33B027a01b1
 Method BLASTX
 NCBI GI g2245096
 BLAST score 216
 E value 1.0e-17
 Match length 78
 % identity 62
 NCBI Description (Z97343) inositol 2-dehydrogenase homolog [Arabidopsis thaliana]

Seq. No. 236221
 Seq. ID uC-gsflnu33B027a02b1
 Method BLASTX
 NCBI GI g4539301
 BLAST score 219
 E value 8.0e-18
 Match length 114
 % identity 38
 NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 236222
 Seq. ID uC-gsflnu33B027a09b1
 Method BLASTX
 NCBI GI g3367534
 BLAST score 526
 E value 9.0e-54
 Match length 139
 % identity 76
 NCBI Description (AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 236223
 Seq. ID uC-gsflnu33B027b12b1
 Method BLASTX
 NCBI GI g1621467
 BLAST score 633
 E value 3.0e-66
 Match length 161

E value 2.0e-50
 Match length 102
 % identity 93
 NCBI Description H+-transporting ATPase (EC 3.6.1.35) (clone PHA1) - potato
 >gi_435003_emb_CAA54046_ (X76536) H(+)-transporting ATPase
 [Solanum tuberosum]

Seq. No. 236229
 Seq. ID uC-gsflnu33B027g02b1
 Method BLASTX
 NCBI GI g1171978
 BLAST score 278
 E value 3.0e-25
 Match length 80
 % identity 18
 NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
 (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
 [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
 poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 236230
 Seq. ID uC-gsflnu33B027h04b1
 Method BLASTX
 NCBI GI g3850818
 BLAST score 390
 E value 7.0e-38
 Match length 90
 % identity 77
 NCBI Description (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
 sativa]

Seq. No. 236231
 Seq. ID uC-gsflnu33B028a04b1
 Method BLASTX
 NCBI GI g2781362
 BLAST score 200
 E value 7.0e-16
 Match length 89
 % identity 23
 NCBI Description (AC003113) F2401.18 [Arabidopsis thaliana]

Seq. No. 236232
 Seq. ID uC-gsflnu33B028b04b1
 Method BLASTX
 NCBI GI g3142292
 BLAST score 543
 E value 1.0e-55
 Match length 125
 % identity 79
 NCBI Description (AC002411) Contains similarity to tetratricopeptide repeat
 protein gb_U46571 from homo sapiens. EST gb_Z47802 and
 gb_Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No. 236233
 Seq. ID uC-gsflnu33B028b08b1
 Method BLASTX
 NCBI GI g1076510

09684016-101000

thaliana]

Seq. No. 236249
 Seq. ID uC-gsflnu33B035a08b1
 Method BLASTX
 NCBI GI g2829918
 BLAST score 312
 E value 1.0e-28
 Match length 123
 % identity 54
 NCBI Description (AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No. 236250
 Seq. ID uC-gsflnu33B035a12b1
 Method BLASTX
 NCBI GI g2281449
 BLAST score 224
 E value 2.0e-18
 Match length 86
 % identity 55
 NCBI Description (U90214) leucine zipper transcription factor TGA2.1 [Nicotiana tabacum]

Seq. No. 236251
 Seq. ID uC-gsflnu33B035b05b1
 Method BLASTX
 NCBI GI g2583108
 BLAST score 243
 E value 4.0e-21
 Match length 70
 % identity 70
 NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 236252
 Seq. ID uC-gsflnu33B035c07b1
 Method BLASTX
 NCBI GI g3738316
 BLAST score 363
 E value 1.0e-34
 Match length 106
 % identity 67
 NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 236253
 Seq. ID uC-gsflnu33B035d07b1
 Method BLASTX
 NCBI GI g2270994
 BLAST score 134
 E value 3.0e-10
 Match length 99
 % identity 42
 NCBI Description (AF004809) Ca²⁺-binding EF hand protein [Glycine max]

Seq. No. 236254
 Seq. ID uC-gsflnu33B035d12b1
 Method BLASTX

Match length 58
 % identity 62
 NCBI Description (AF013293) contains weak similarity to *S. cerevisiae* BOB1 protein (PIR:S45444) [*Arabidopsis thaliana*]

Seq. No. 236265
 Seq. ID uC-gsflnu33B037d06b1
 Method BLASTX
 NCBI GI g2342725
 BLAST score 309
 E value 3.0e-28
 Match length 141
 % identity 48
 NCBI Description (AC002341) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 236266
 Seq. ID uC-gsflnu33B037e11b1
 Method BLASTX
 NCBI GI g4262228
 BLAST score 368
 E value 2.0e-35
 Match length 111
 % identity 74
 NCBI Description (AC006200) putative receptor protein kinase [*Arabidopsis thaliana*]

Seq. No. 236267
 Seq. ID uC-gsflnu33B037f01b1
 Method BLASTX
 NCBI GI g3024516
 BLAST score 317
 E value 8.0e-45
 Match length 118
 % identity 86
 NCBI Description RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong similarity to *A. thaliana* ara-2 (gb_ATHARA2). ESTs gb_ATTS2483, gb_ATTS2484, gb_AA042159 come from this gene. [*Arabidopsis thaliana*] >gi_2231303 (U74669) ras-related small GTPase [*Arabidopsis thaliana*]

Seq. No. 236268
 Seq. ID uC-gsflnu33B037h09b1
 Method BLASTX
 NCBI GI g2281090
 BLAST score 307
 E value 1.0e-28
 Match length 75
 % identity 84
 NCBI Description (AC002333) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 236269
 Seq. ID uC-gsflnu33B046a09b1
 Method BLASTX
 NCBI GI g4455323
 BLAST score 143
 E value 4.0e-09
 Match length 63


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Seq. No.      236280
Seq. ID       uC-gsflnu33B049d04b1
Method        BLASTX
NCBI GI       g464981
BLAST score    393
E value       4.0e-38
Match length   74
% identity     99
NCBI Description  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
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Seq. No.      236281
Seq. ID       uC-gsflnu33B049e06b1
Method        BLASTX
NCBI GI       g416641
BLAST score   229
E value       2.0e-19
Match length  48
% identity    85
NCBI Description  INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG4
                >gi_287568_dbj_BAA03309_(D14413) ORF [Vigna radiata]
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Seq. No.          236282
Seq. ID           uC-gsflnu33B049e08b1
Method            BLASTX
NCBI GI           g4100433
BLAST score       240
E value           2.0e-20
Match length      72
% identity        56
NCBI Description   (AF000378) beta-glucosidase [Glycine max]
```

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Seq. No.      236283
Seq. ID       uC-gsflnu33B049f01b1
Method        BLASTX
NCBI GI       g1707015
BLAST score    345
E value        9.0e-33
Match length   101
% identity     65
NCBI Description (U78721) protein phosphatase 2C isolog [Arabidopsis
                thaliana]
```

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Seq. No.          236284
Seq. ID           uC-gsflnu33B049f09b1
Method            BLASTX
NCBI GI           g3789940
BLAST score       216
E value           5.0e-18
Match length      47
% identity        23
NCBI Description   (AF093504) tetra-ubiquitin [Saccharum hybrid cultivar
                  H32-8560]
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Seq. No. 236285

09584016-101000

Seq. No. 236301
Seq. ID uC-gsflnu33B051f03b1
Method BLASTX
NCBI GI g3914430
BLAST score 205
E value 2.0e-16
Match length 64
% identity 61
NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No. 236302
Seq. ID uC-gsflnu33B051g02b1
Method BLASTX
NCBI GI g548441
BLAST score 250
E value 5.0e-22
Match length 45
% identity 98
NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT >gi_486805_pir_S35502 phosphoprotein phosphatase (EC 3.1.3.16) 2A - alfalfa >gi_287811_emb_CAA49849_ (X70399) phosphoprotein phosphatase type 2A [Medicago sativa]

Seq. No. 236303
Seq. ID uC-gsflnu33B051g07b1
Method BLASTX
NCBI GI g538067
BLAST score 164
E value 1.0e-11
Match length 90
% identity 44
NCBI Description (M77661) putative pol polyprotein [Magnaporthe grisea]

Seq. No. 236304
Seq. ID uC-gsflnu33B051h12b1
Method BLASTX
NCBI GI g1076402
BLAST score 159
E value 9.0e-11
Match length 112
% identity 38
NCBI Description S-like ribonuclease RNS2 - Arabidopsis thaliana

Seq. No. 236305
Seq. ID uC-gsflnu33B055a06b1
Method BLASTX
NCBI GI g2104536
BLAST score 263
E value 4.0e-23
Match length 65
% identity 69
NCBI Description (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

SECRET

Seq. No. 236336

Seq. No. 236346
 Seq. ID uC-gsflnu33B059f09b1
 Method BLASTX
 NCBI GI g1345642
 BLAST score 250
 E value 1.0e-21
 Match length 64
 % identity 78
 NCBI Description FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450 75A1) (CYPLXXVA1) >gi_629710_pir_S38985 flavonoid 3',5'-hydroxylase Hfl - garden petunia >gi_311656_emb_CAA80266_(Z22545) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi_1853972_dbj_BAA03438_(D14588) flavonoid-3',5'-hydroxylase [Petunia x hybrida] >gi_3426337 (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi_738772_prf_2001426B flavonoid 3',5'-hydroxylase [Petunia x hybrida]

Seq. No. 236347
 Seq. ID uC-gsflnu33B059f10b1
 Method BLASTX
 NCBI GI g127041
 BLAST score 283
 E value 3.0e-25
 Match length 53
 % identity 92
 NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) ~ >gi_81647_pir_JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No. 236348
 Seq. ID uC-gsflnu33B059g03b1
 Method BLASTX
 NCBI GI g872116
 BLAST score 341
 E value 3.0e-32
 Match length 74
 % identity 46
 NCBI Description (X79770) sti (stress inducible protein) [Glycine max]

Seq. No. 236349
 Seq. ID uC-gsflnu33B059g04b1
 Method BLASTX
 NCBI GI g3668089
 BLAST score 474
 E value 1.0e-47
 Match length 134
 % identity 67
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 236350
 Seq. ID uC-gsflnu33B060a08b1
 Method BLASTX
 NCBI GI g4063748

% identity 75
 NCBI Description (AL035440) Avr9 elicitor response like protein [Arabidopsis thaliana]

Seq. No. 236356
 Seq. ID uC-gsflnu33B060f12b1
 Method BLASTX
 NCBI GI g167367
 BLAST score 227
 E value 7.0e-19
 Match length 44
 % identity 100
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 236357
 Seq. ID uC-gsflnu33B060g10b1
 Method BLASTX
 NCBI GI g4105696
 BLAST score 576
 E value 1.0e-59
 Match length 116
 % identity 93
 NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No. 236358
 Seq. ID uC-gsflnu33B060h07b1
 Method BLASTX
 NCBI GI g130972
 BLAST score 138
 E value 7.0e-09
 Match length 61
 % identity 49
 NCBI Description PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
 >gi_99952_pir_S10186 pyrroline-5-carboxylate reductase (EC
 1.5.1.2) - soybean >gi_18724_emb_CAA34401_ (X16352)
 pyrroline-5-carboxylate reductase (AA 1- 274) [Glycine max]

Seq. No. 236359
 Seq. ID uC-gsflnu33B061a07b1
 Method BLASTX
 NCBI GI g1915974
 BLAST score 254
 E value 3.0e-22
 Match length 58
 % identity 84
 NCBI Description (U62329) fructokinase [Lycopersicon esculentum] >gi_2102693
 (U64818) fructokinase [Lycopersicon esculentum]

Seq. No. 236360
 Seq. ID uC-gsflnu33B061b12b1
 Method BLASTX
 NCBI GI g135915
 BLAST score 224
 E value 1.0e-18
 Match length 76
 % identity 58
 NCBI Description PATHOGENESIS-RELATED PROTEIN 5 PRECURSOR (PR-5)

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34264

Match length 104
 % identity 53
 NCBI Description (AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No. 236371
 Seq. ID uC-gsflnu33B062a11b1
 Method BLASTX
 NCBI GI g3941480
 BLAST score 361
 E value 6.0e-35
 Match length 71
 % identity 93
 NCBI Description (AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No. 236372
 Seq. ID uC-gsflnu33B062b02b1
 Method BLASTX
 NCBI GI g2583110
 BLAST score 162
 E value 4.0e-11
 Match length 62
 % identity 60
 NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]

Seq. No. 236373
 Seq. ID uC-gsflnu33B062b07b1
 Method BLASTX
 NCBI GI g4539292
 BLAST score 337
 E value 7.0e-32
 Match length 71
 % identity 86
 NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 236374
 Seq. ID uC-gsflnu33B062b10b1
 Method BLASTX
 NCBI GI g544075
 BLAST score 304
 E value 1.0e-42
 Match length 111
 % identity 53
 NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi_486768_pir_S35312 coatomer complex chain beta' - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop [Bos taurus]

Seq. No. 236375
 Seq. ID uC-gsflnu33B062c12b1
 Method BLASTX
 NCBI GI g860712
 BLAST score 193
 E value 6.0e-30
 Match length 86

% identity 70
 NCBI Description (U28735) coded for by C. elegans cDNA cm06e4; coded for by C. elegans cDNA CEESP39F; coded for by C. elegans cDNA CEESR26F; coded for by C. elegans cDNA CEESX83F; coded for by C. elegans cDNA yk16e9.3; coded for by C. elegans cDNA yk16e9.5; c

Seq. No. 236376
 Seq. ID uC-gsflnu33B062d01b1
 Method BLASTX
 NCBI GI g3415126
 BLAST score 181
 E value 1.0e-13
 Match length 91
 % identity 41
 NCBI Description (AF081678) phenylcoumaran benzylic ether reductase [Pinus taeda]

Seq. No. 236377
 Seq. ID uC-gsflnu33B062e01b1
 Method BLASTX
 NCBI GI g1050849
 BLAST score 204
 E value 4.0e-16
 Match length 110
 % identity 40
 NCBI Description (X83742) MAP kinase phosphatase [Xenopus laevis]

Seq. No. 236378
 Seq. ID uC-gsflnu33B062f02b1
 Method BLASTX
 NCBI GI g4263522
 BLAST score 261
 E value 6.0e-23
 Match length 97
 % identity 25
 NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236379
 Seq. ID uC-gsflnu33B062f04b1
 Method BLASTX
 NCBI GI g2369714
 BLAST score 143
 E value 5.0e-09
 Match length 36
 % identity 81
 NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 236380
 Seq. ID uC-gsflnu33B062h01b1
 Method BLASTX
 NCBI GI g3005576
 BLAST score 176
 E value 7.0e-28
 Match length 89
 % identity 69
 NCBI Description (AF047718) putative high affinity nitrate transporter;

09584016-101000

GmNRT2 [Glycine max]

Seq. No. 236381
 Seq. ID uC-gsflnu33B062h07b1
 Method BLASTX
 NCBI GI g4559380
 BLAST score 349
 E value 3.0e-33
 Match length 99
 % identity 63
 NCBI Description (AC006526) putative auxin-responsive GH3 protein
 [Arabidopsis thaliana]

Seq. No. 236382
 Seq. ID uC-gsflnu33B063a04b1
 Method BLASTX
 NCBI GI g3152585
 BLAST score 224
 E value 2.0e-18
 Match length 97
 % identity 55
 NCBI Description (AC002986) Contains similarity to auxin-induced protein
 TM018A10.6 from A. thaliana BAC gb_AF013294. [Arabidopsis
 thaliana]

Seq. No. 236383
 Seq. ID uC-gsflnu33B063b10b1
 Method BLASTX
 NCBI GI g3250675
 BLAST score 368
 E value 9.0e-42
 Match length 124
 % identity 65
 NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 236384
 Seq. ID uC-gsflnu33B063c05b1
 Method BLASTX
 NCBI GI g1174199
 BLAST score 189
 E value 3.0e-14
 Match length 76
 % identity 55
 NCBI Description (U44760) S25-PR6 [Nicotiana tabacum]

Seq. No. 236385
 Seq. ID uC-gsflnu33B063e03b1
 Method BLASTX
 NCBI GI g1402912
 BLAST score 470
 E value 4.0e-47
 Match length 121
 % identity 74
 NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 236386
 Seq. ID uC-gsflnu33B063f11b1

Method BLASTX
 NCBI GI g4454025
 BLAST score 327
 E value 2.0e-30
 Match length 125
 % identity 48
 NCBI Description (AL035394) putative cellulase [Arabidopsis thaliana]

Seq. No. 236387
 Seq. ID uC-gsflnu33B063f12b1
 Method BLASTX
 NCBI GI g4522005
 BLAST score 180
 E value 4.0e-13
 Match length 136
 % identity 33
 NCBI Description (AC007069) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 236388
 Seq. ID uC-gsflnu33B063g02b1
 Method BLASTX
 NCBI GI g4097579
 BLAST score 257
 E value 2.0e-22
 Match length 72
 % identity 68
 NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 236389
 Seq. ID uC-gsflnu33B063g10b1
 Method BLASTX
 NCBI GI g4115377
 BLAST score 203
 E value 6.0e-16
 Match length 46
 % identity 80
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 236390
 Seq. ID uC-gsflnu33B063h02b1
 Method BLASTX
 NCBI GI g166410
 BLAST score 164
 E value 3.0e-19
 Match length 64
 % identity 69
 NCBI Description (L07291) Alfin-1 [Medicago sativa]

Seq. No. 236391
 Seq. ID uC-gsflnu33B063h03b1
 Method BLASTX
 NCBI GI g4263517
 BLAST score 146
 E value 1.0e-12
 Match length 63
 % identity 54

09634016-101000

NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana]

Seq. No. 236392
Seq. ID uC-gsflnu33B064b01b1
Method BLASTX
NCBI GI g3805956
BLAST score 266
E value 3.0e-29
Match length 72
% identity 89
NCBI Description (Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No. 236393
Seq. ID uC-gsflnu33B064b09b1
Method BLASTX
NCBI GI g2980795
BLAST score 262
E value 4.0e-23
Match length 86
% identity 58
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 236394
Seq. ID uC-gsflnu33B064c01b1
Method BLASTX
NCBI GI g2459440
BLAST score 434
E value 5.0e-43
Match length 129
% identity 64
NCBI Description (AC002332) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 236395
Seq. ID uC-gsflnu33B064d12b1
Method BLASTX
NCBI GI g4371285
BLAST score 194
E value 6.0e-15
Match length 95
% identity 48
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236396
Seq. ID uC-gsflnu33B064e01b1
Method BLASTX
NCBI GI g3249105
BLAST score 237
E value 2.0e-20
Match length 68
% identity 69
NCBI Description (AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 236397

Seq. ID uC-gsflnu33B064e07b1
 Method BLASTX
 NCBI GI g2738982
 BLAST score 421
 E value 2.0e-41
 Match length 137
 % identity 61
 NCBI Description (AF022157) CYP71A10 [Glycine max]

Seq. No. 236398
 Seq. ID uC-gsflnu33B064f01b1
 Method BLASTX
 NCBI GI g2911067
 BLAST score 446
 E value 2.0e-44
 Match length 100
 % identity 86
 NCBI Description (AL021960) UV-damaged DNA-binding protein- like
 [Arabidopsis thaliana]

Seq. No. 236399
 Seq. ID uC-gsflnu33B064g04b1
 Method BLASTX
 NCBI GI g1488255
 BLAST score 323
 E value 1.0e-30
 Match length 75
 % identity 88
 NCBI Description (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
 >gi_2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase
 (FAH1) [Arabidopsis thaliana] >gi_3925365 (AF068574)
 ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No. 236400
 Seq. ID uC-gsflnu33B064g07b1
 Method BLASTX
 NCBI GI g1730057
 BLAST score 173
 E value 2.0e-12
 Match length 41
 % identity 73
 NCBI Description PROBABLE SERINE/THREONINE-PROTEIN KINASE YNR047W
 >gi_2131975_pir_S63378 hypothetical protein YNR047w -
 yeast (Saccharomyces cerevisiae) >gi_1302558_emb_CAA96328_
 (Z71662) ORF YNR047w [Saccharomyces cerevisiae]

Seq. No. 236401
 Seq. ID uC-gsflnu33B064g11b1
 Method BLASTX
 NCBI GI g2388994
 BLAST score 401
 E value 3.0e-39
 Match length 118
 % identity 64
 NCBI Description (Z98981) hypothetical gtp-binding protein associated
 [Schizosaccharomyces pombe]

Method BLASTX
 NCBI GI g4512670
 BLAST score 216
 E value 2.0e-17
 Match length 77
 % identity 44
 NCBI Description (AC006931) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 236408
 Seq. ID uC-gsflnu33B066e05b1
 Method BLASTX
 NCBI GI g2398523
 BLAST score 220
 E value 6.0e-18
 Match length 88
 % identity 61
 NCBI Description (Y13721) Transcription factor [Arabidopsis thaliana]

Seq. No. 236409
 Seq. ID uC-gsflnu33B066f02b1
 Method BLASTX
 NCBI GI g3355780
 BLAST score 150
 E value 8.0e-10
 Match length 28
 % identity 86
 NCBI Description (AJ004997) expansin18 [Lycopersicon esculentum]

Seq. No. 236410
 Seq. ID uC-gsflnu33B066f08b1
 Method BLASTX
 NCBI GI g2522227
 BLAST score 149
 E value 2.0e-09
 Match length 79
 % identity 43
 NCBI Description (AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]

Seq. No. 236411
 Seq. ID uC-gsflnu33B066g12b1
 Method BLASTX
 NCBI GI g4539292
 BLAST score 452
 E value 4.0e-45
 Match length 96
 % identity 86
 NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 236412
 Seq. ID uC-gsflnu33B066h01b1
 Method BLASTX
 NCBI GI g3947719
 BLAST score 249
 E value 3.0e-21
 Match length 53

% identity 92
 NCBI Description (AJ012653) ribosomal protein S28 [Prunus persica]
 >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28
 [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655)
 ribosomal protein S28 [Prunus persica]

Seq. No. 236413
 Seq. ID uC-gsflnu33B066h08b1
 Method BLASTX
 NCBI GI g3250697
 BLAST score 252
 E value 7.0e-22
 Match length 56
 % identity 82
 NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 236414
 Seq. ID uC-gsflnu33B066h09b1
 Method BLASTX
 NCBI GI g3335347
 BLAST score 479
 E value 2.0e-48
 Match length 104
 % identity 77
 NCBI Description (AC004512) Contains similarity to ARI, RING finger protein
 gb_X98309 from Drosophila melanogaster. ESTs gb_T44383,
 gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and
 gb_AA042359 come from this gene. [Arabidopsis thaliana]

Seq. No. 236415
 Seq. ID uC-gsflnu33B068e01b1
 Method BLASTX
 NCBI GI g1518540
 BLAST score 615
 E value 3.0e-64
 Match length 124
 % identity 89
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 236416
 Seq. ID uC-gsflnu33B068e12b1
 Method BLASTX
 NCBI GI g584893
 BLAST score 182
 E value 5.0e-14
 Match length 50
 % identity 66
 NCBI Description SERINE CARBOXYPEPTIDASE III PRECURSOR
 >gi_283002_pir_S22530 carboxypeptidase III (EC 3.4.16.-) -
 rice >gi_218153_dbj_BAA01757_ (D10985) serine
 carboxypeptidase III [Oryza sativa]

Seq. No. 236417
 Seq. ID uC-gsflnu33B068f01b1
 Method BLASTX
 NCBI GI g710626
 BLAST score 149

Match length 35
 % identity 94
 NCBI Description (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]

Seq. No. 236428
 Seq. ID uC-gsflnu33B071d08b1
 Method BLASTX
 NCBI GI g4102839
 BLAST score 240
 E value 3.0e-27
 Match length 148
 % identity 47
 NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 236429
 Seq. ID uC-gsflnu33B071e12b1
 Method BLASTX
 NCBI GI g531389
 BLAST score 138
 E value 2.0e-10
 Match length 70
 % identity 51
 NCBI Description (U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq. No. 236430
 Seq. ID uC-gsflnu33B071f01b1
 Method BLASTX
 NCBI GI g3452263
 BLAST score 155
 E value 3.0e-10
 Match length 31
 % identity 90
 NCBI Description (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis thaliana]

Seq. No. 236431
 Seq. ID uC-gsflnu33B071h03b1
 Method BLASTX
 NCBI GI g2541876
 BLAST score 177
 E value 6.0e-13
 Match length 92
 % identity 45
 NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No. 236432
 Seq. ID uC-gsflnu33B071h10b1
 Method BLASTX
 NCBI GI g3492806
 BLAST score 403
 E value 2.0e-39
 Match length 103
 % identity 77
 NCBI Description (AJ225045) adventitious rooting related oxygenase [Malus domestica]

E value 4.0e-15
 Match length 38
 % identity 84
 NCBI Description (U71244) pathogenesis-related group 5 protein [Brassica rapa]

Seq. No. 236439
 Seq. ID uC-gsflnu33B073c07b1
 Method BLASTX
 NCBI GI g4193388
 BLAST score 210
 E value 2.0e-17
 Match length 45
 % identity 89
 NCBI Description (AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No. 236440
 Seq. ID uC-gsflnu33B073f06b1
 Method BLASTX
 NCBI GI g4531434
 BLAST score 160
 E value 2.0e-11
 Match length 40
 % identity 70
 NCBI Description (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No. 236441
 Seq. ID uC-gsflnu33B074d05b1
 Method BLASTX
 NCBI GI g2129597
 BLAST score 457
 E value 9.0e-46
 Match length 93
 % identity 92
 NCBI Description glutamate dehydrogenase 1 - Arabidopsis thaliana
 >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No. 236442
 Seq. ID uC-gsflnu33B074d11b1
 Method BLASTX
 NCBI GI g4432855
 BLAST score 197
 E value 2.0e-15
 Match length 102
 % identity 50
 NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 236443
 Seq. ID uC-gsflnu33B074e06b1
 Method BLASTX
 NCBI GI g2708743
 BLAST score 144
 E value 6.0e-09
 Match length 139

Seq. ID uC-gsflnu33B074h07b1
 Method BLASTX
 NCBI GI g3695059
 BLAST score 283
 E value 3.0e-25
 Match length 81
 % identity 73
 NCBI Description (AF064787) rac GTPase activating protein 1 [Lotus japonicus]

Seq. No. 236450
 Seq. ID uC-gsflnu33B074h12b1
 Method BLASTX
 NCBI GI g2760835
 BLAST score 622
 E value 5.0e-65
 Match length 148
 % identity 80
 NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]

Seq. No. 236451
 Seq. ID uC-gsflnu33B075b03b1
 Method BLASTX
 NCBI GI g1707955
 BLAST score 477
 E value 4.0e-48
 Match length 96
 % identity 92
 NCBI Description GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1 (GLUTAMATE--AMMONIA LIGASE) >gi_1134896_emb_CAA63981_ (X94320) glutamine synthetase [Vitis vinifera]

Seq. No. 236452
 Seq. ID uC-gsflnu33B075b04b1
 Method BLASTX
 NCBI GI g1361983
 BLAST score 365
 E value 4.0e-35
 Match length 105
 % identity 70
 NCBI Description ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No. 236453
 Seq. ID uC-gsflnu33B075c06b1
 Method BLASTX
 NCBI GI g3142296
 BLAST score 252
 E value 6.0e-22
 Match length 86
 % identity 56
 NCBI Description (AC002411) Contains similarity to hypothetical mitochondrial import receptor subunit gb_298597 from S. pombe. ESTs gb_T45575 and gb_Z26435 and gb_AA394576 come from this gene. [Arabidopsis thaliana]

Seq. No. 236454

NCBI GI g2642428
 BLAST score 298
 E value 5.0e-27
 Match length 118
 % identity 48
 NCBI Description (AC002391) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No. 236460
 Seq. ID uC-gsflnu33B075g04b1
 Method BLASTX
 NCBI GI g2454629
 BLAST score 272
 E value 1.0e-24
 Match length 62
 % identity 82
 NCBI Description (AF019559) cytosolic glutamine synthetase; GS1 [Daucus carota]

Seq. No. 236461
 Seq. ID uC-gsflnu33B075g09b1
 Method BLASTX
 NCBI GI g4539437
 BLAST score 195
 E value 5.0e-15
 Match length 42
 % identity 83
 NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 236462
 Seq. ID uC-gsflnu33B075h04b1
 Method BLASTX
 NCBI GI g3250680
 BLAST score 513
 E value 3.0e-52
 Match length 121
 % identity 82
 NCBI Description (AL024486) aspartate kinase-homoserine dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No. 236463
 Seq. ID uC-gsflnu33B076e06b1
 Method BLASTX
 NCBI GI g1408471
 BLAST score 181
 E value 3.0e-13
 Match length 40
 % identity 88
 NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No. 236464
 Seq. ID uC-gsflnu33B076e12b1
 Method BLASTX
 NCBI GI g3132475
 BLAST score 176

BLAST score 266
 E value 2.0e-23
 Match length 106
 % identity 53
 NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 236480
 Seq. ID uC-gsflnu33B078h10b1
 Method BLASTX
 NCBI GI g3559811
 BLAST score 246
 E value 7.0e-21
 Match length 60
 % identity 78
 NCBI Description (AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No. 236481
 Seq. ID uC-gsflnu33B079d01b1
 Method BLASTX
 NCBI GI g2586123
 BLAST score 463
 E value 2.0e-46
 Match length 100
 % identity 87
 NCBI Description (U89511) b-keto acyl reductase [Allium porrum]

Seq. No. 236482
 Seq. ID uC-gsflnu33B079d05b1
 Method BLASTX
 NCBI GI g4580461
 BLAST score 286
 E value 3.0e-26
 Match length 59
 % identity 92
 NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 236483
 Seq. ID uC-gsflnu33B079e06b1
 Method BLASTX
 NCBI GI g117188
 BLAST score 411
 E value 2.0e-40
 Match length 127
 % identity 57
 NCBI Description CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2)
 >gi_81423_pir_A35867 cytochrome P450 71A1 - avocado

Seq. No. 236484
 Seq. ID uC-gsflnu33B079f03b1
 Method BLASTX
 NCBI GI g123554
 BLAST score 142
 E value 3.0e-09
 Match length 33
 % identity 79
 NCBI Description 18.1 KD CLASS I HEAT SHOCK PROTEIN >gi_99978_pir_S16248
 heat shock protein 18 (clone pMsHsp18.1) - alfalfa

Seq. No. 236495
 Seq. ID uC-gsflnu33B082a11b1
 Method BLASTX
 NCBI GI g1076387
 BLAST score 338
 E value 8.0e-32
 Match length 89
 % identity 69
 NCBI Description protein kinase homolog - Arabidopsis thaliana
 >gi_717180_emb_CAA55866_(X79279) protein kinase homologous
 to shaggy and glycogen synthase kinase-3 [Arabidopsis
 thaliana]

Seq. No. 236496
 Seq. ID uC-gsflnu33B082c08b1
 Method BLASTX
 NCBI GI g1755166
 BLAST score 381
 E value 9.0e-37
 Match length 102
 % identity 74
 NCBI Description (U75194) germin-like protein [Arabidopsis thaliana]

Seq. No. 236497
 Seq. ID uC-gsflnu33B082d11b1
 Method BLASTX
 NCBI GI g1171579
 BLAST score 386
 E value 1.0e-46
 Match length 129
 % identity 71
 NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 236498
 Seq. ID uC-gsflnu33B082e10b1
 Method BLASTX
 NCBI GI g3337361
 BLAST score 431
 E value 8.0e-43
 Match length 99
 % identity 79
 NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 236499
 Seq. ID uC-gsflnu33B082f11b1
 Method BLASTX
 NCBI GI g4220527
 BLAST score 611
 E value 1.0e-63
 Match length 131
 % identity 82
 NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 236500
 Seq. ID uC-gsflnu33B082g10b1
 Method BLASTX
 NCBI GI g2827548

BLAST score 222
 E value 5.0e-28
 Match length 137
 % identity 50
 NCBI Description (AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No. 236501
 Seq. ID uC-gsflnu33B082g11b1
 Method BLASTX
 NCBI GI g1749596
 BLAST score 169
 E value 8.0e-12
 Match length 42
 % identity 69
 NCBI Description (D89194) similar to Rat ATP citrate-lyase, SWISS-PROT Accession Number P16638 [Schizosaccharomyces pombe]

Seq. No. 236502
 Seq. ID uC-gsflnu33B082h02b1
 Method BLASTX
 NCBI GI g4539350
 BLAST score 266
 E value 3.0e-38
 Match length 113
 % identity 71
 NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 236503
 Seq. ID uC-gsflnu33B083a02b1
 Method BLASTX
 NCBI GI g4337189
 BLAST score 237
 E value 6.0e-20
 Match length 74
 % identity 55
 NCBI Description (AC006403) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No. 236504
 Seq. ID uC-gsflnu33B083a04b1
 Method BLASTX
 NCBI GI g2842477
 BLAST score 237
 E value 4.0e-20
 Match length 72
 % identity 65
 NCBI Description (AL021749) copper-binding protein-like [Arabidopsis thaliana]

Seq. No. 236505
 Seq. ID uC-gsflnu33B083b03b1
 Method BLASTX
 NCBI GI g1076708
 BLAST score 375
 E value 4.0e-36
 Match length 75

E value 4.0e-13
 Match length 60
 % identity 52
 NCBI Description (Z97341) limonene cyclase [Arabidopsis thaliana]

Seq. No. 236511
 Seq. ID uC-gsflnu33B084c10b1
 Method BLASTX
 NCBI GI g730645
 BLAST score 516
 E value 1.0e-52
 Match length 111
 % identity 90
 NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir_S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_(Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_(AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No. 236512
 Seq. ID uC-gsflnu33B084d03b1
 Method BLASTX
 NCBI GI g4218011
 BLAST score 150
 E value 1.0e-09
 Match length 53
 % identity 58
 NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_(AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 236513
 Seq. ID uC-gsflnu33B084e03b1
 Method BLASTX
 NCBI GI g2739381
 BLAST score 339
 E value 7.0e-32
 Match length 112
 % identity 60
 NCBI Description (AC002505) putative patatin [Arabidopsis thaliana]

Seq. No. 236514
 Seq. ID uC-gsflnu33B084e11b1
 Method BLASTX
 NCBI GI g2618684
 BLAST score 309
 E value 3.0e-28
 Match length 95
 % identity 62
 NCBI Description (AC002510) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase [Arabidopsis thaliana] >gi_3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate

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N-acetylglucosaminophosphotransferase [Arabidopsis thaliana]

Seq. No. 236515
 Seq. ID uC-gsflnu33B084f05b1
 Method BLASTX
 NCBI GI g4415938
 BLAST score 192
 E value 4.0e-27
 Match length 83
 % identity 72
 NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

Seq. No. 236516
 Seq. ID uC-gsflnu33B084f09b1
 Method BLASTX
 NCBI GI g3759177
 BLAST score 161
 E value 6.0e-11
 Match length 47
 % identity 72
 NCBI Description (AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi_3759179_dbj_BAA33807_ (AB018409) 3-phosphoserine phosphatase [Arabidopsis thaliana]

Seq. No. 236517
 Seq. ID uC-gsflnu33B084h06b1
 Method BLASTX
 NCBI GI g3252815
 BLAST score 290
 E value 4.0e-26
 Match length 74
 % identity 78
 NCBI Description (AC004705) vacuolar sorting receptor-like protein [Arabidopsis thaliana] >gi_3810588 (AC005398) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No. 236518
 Seq. ID uC-gsflnu33B085d05b1
 Method BLASTX
 NCBI GI g4580461
 BLAST score 286
 E value 3.0e-26
 Match length 59
 % identity 92
 NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 236519
 Seq. ID uC-gsflnu33B085h03b1
 Method BLASTX
 NCBI GI g3080447
 BLAST score 161
 E value 5.0e-20
 Match length 117
 % identity 54
 NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 236520
 Seq. ID uC-gsflnu33B085h07b1
 Method BLASTX
 NCBI GI g3935168
 BLAST score 250
 E value 2.0e-21
 Match length 96
 % identity 58
 NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 236521
 Seq. ID uC-gsflnu33B088a02b1
 Method BLASTX
 NCBI GI g3176684
 BLAST score 360
 E value 2.0e-34
 Match length 107
 % identity 67
 NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside transporter 1 gb_U81375 from Homo sapiens. ESTs gb_N65317, gb_T20785, gb_AA586285 and gb_AA712578 come from this gene. [Arabidopsis thaliana]

Seq. No. 236522
 Seq. ID uC-gsflnu33B088a05b1
 Method BLASTX
 NCBI GI g3540219
 BLAST score 187
 E value 2.0e-14
 Match length 52
 % identity 62
 NCBI Description (D87686) KIAA0017 protein [Homo sapiens]

Seq. No. 236523
 Seq. ID uC-gsflnu33B088b05b1
 Method BLASTX
 NCBI GI g1946279
 BLAST score 287
 E value 7.0e-26
 Match length 102
 % identity 47
 NCBI Description (Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]

Seq. No. 236524
 Seq. ID uC-gsflnu33B088b11b1
 Method BLASTX
 NCBI GI g3915601
 BLAST score 257
 E value 1.0e-22
 Match length 78
 % identity 63
 NCBI Description ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (A1 38 KD SUBUNIT) (RF-C 38 KD SUBUNIT) (RFC38) >gi_1498259 (L07541) replication factor C, 38-kDa subunit [Homo sapiens] >gi_4506489_ref_NP_002906.1_pRFC3_ replication factor C (activator 1) 3 (38kD)

Seq. No.	236525
Seq. ID	uC-gsflnu33B088c02b1
Method	BLASTX
NCBI GI	g407942
BLAST score	218
E value	1.0e-17
Match length	53
% identity	70
NCBI Description	(U02496) epoxide hydrolase [Solanum tuberosum]
Seq. No.	236526
Seq. ID	uC-gsflnu33B088d05b1
Method	BLASTX
NCBI GI	g3461820
BLAST score	270
E value	2.0e-24
Match length	60
% identity	73
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.	236527
Seq. ID	uC-gsflnu33B088d06b1
Method	BLASTX
NCBI GI	g3702321
BLAST score	447
E value	9.0e-45
Match length	98
% identity	50
NCBI Description	(AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]
Seq. No.	236528
Seq. ID	uC-gsflnu33B088e10b1
Method	BLASTX
NCBI GI	g3757515
BLAST score	189
E value	2.0e-14
Match length	66
% identity	59
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]
Seq. No.	236529
Seq. ID	uC-gsflnu33B088e12b1
Method	BLASTX
NCBI GI	g231757
BLAST score	625
E value	3.0e-65
Match length	146
% identity	84
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_99653_pir_S18568 lignin-bispecific O-methyltransferase (EC 2.1.1.-) - quaking aspen >gi_20951_emb_CAA44006_(X62096) lignin bispecific acid/5-hydroxyferulic acid methyltransferase [Populus tremuloides] >gi_2226267 (U13171) caffeic

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acid/5-hydroxyferulic acid O-methyltransferase [Populus tremuloides]

Seq. No. 236530
Seq. ID uC-gsflnu33B088f07b1
Method BLASTX
NCBI GI g3135274
BLAST score 196
E value 3.0e-15
Match length 45
% identity 82
NCBI Description (AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No. 236531
Seq. ID uC-gsflnu33B088f08b1
Method BLASTX
NCBI GI g3600048
BLAST score 409
E value 5.0e-45
Match length 115
% identity 77
NCBI Description (AF080120) similar to hypothetical proteins in Schizosaccharomyces pombe (GB:Z98533) and C. elegans (GB:Z48334 and Z78419) [Arabidopsis thaliana]

Seq. No. 236532
Seq. ID uC-gsflnu33B088g07b1
Method BLASTX
NCBI GI g3643604
BLAST score 225
E value 8.0e-19
Match length 81
% identity 56
NCBI Description (AC005395) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 236533
Seq. ID uC-gsflnu33B088h03b1
Method BLASTX
NCBI GI g3702334
BLAST score 185
E value 7.0e-14
Match length 116
% identity 41
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236534
Seq. ID uC-gsflnu33B088h04b1
Method BLASTX
NCBI GI g4193382
BLAST score 392
E value 4.0e-38
Match length 86
% identity 84
NCBI Description (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
>gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis

09654016-101000

thaliana]

Seq. No. 236535
 Seq. ID uC-gsflnu33B089a12b1
 Method BLASTX
 NCBI GI g4455190
 BLAST score 266
 E value 2.0e-23
 Match length 69
 % identity 80
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 236536
 Seq. ID uC-gsflnu33B089b01b1
 Method BLASTX
 NCBI GI g3746060
 BLAST score 463
 E value 2.0e-46
 Match length 116
 % identity 78
 NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 236537
 Seq. ID uC-gsflnu33B089b04b1
 Method BLASTX
 NCBI GI g2465923
 BLAST score 181
 E value 7.0e-14
 Match length 47
 % identity 68
 NCBI Description (AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 236538
 Seq. ID uC-gsflnu33B089b06b1
 Method BLASTX
 NCBI GI g1762939
 BLAST score 136
 E value 1.0e-08
 Match length 35
 % identity 69
 NCBI Description (U66266) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No. 236539
 Seq. ID uC-gsflnu33B089b09b1
 Method BLASTX
 NCBI GI g3080452
 BLAST score 321
 E value 4.0e-30
 Match length 88
 % identity 67
 NCBI Description (AL022605) putative L-ascorbate oxidase [Arabidopsis thaliana]

Seq. No. 236540
 Seq. ID uC-gsflnu33B089c05b1

Method BLASTX
 NCBI GI g1169782
 BLAST score 506
 E value 1.0e-51
 Match length 112
 % identity 88
 NCBI Description FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No. 236541
 Seq. ID uC-gsflnu33B089c12b1
 Method BLASTX
 NCBI GI g3935148
 BLAST score 190
 E value 2.0e-14
 Match length 57
 % identity 68
 NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No. 236542
 Seq. ID uC-gsflnu33B089d05b1
 Method BLASTX
 NCBI GI g3212863
 BLAST score 182
 E value 5.0e-14
 Match length 42
 % identity 83
 NCBI Description (AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No. 236543
 Seq. ID uC-gsflnu33B089d12b1
 Method BLASTX
 NCBI GI g130181
 BLAST score 180
 E value 2.0e-13
 Match length 37
 % identity 86
 NCBI Description PHYTOCHROME A TYPE 3 (AP3) >gi_82335_pir_S00096
 phytochrome 3 - oat >gi_16111_emb_CAA26999_ (X03242)
 phytochrome type 3 (aa 1-1129) [Avena sativa]

Seq. No. 236544
 Seq. ID uC-gsflnu33B089e04b1
 Method BLASTX
 NCBI GI g1663722
 BLAST score 321
 E value 6.0e-30
 Match length 81
 % identity 70
 NCBI Description (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 236545
 Seq. ID uC-gsflnu33B089f04b1
 Method BLASTX
 NCBI GI g167367
 BLAST score 153

E value 1.0e-10
 Match length 49
 % identity 61
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 236546
 Seq. ID uC-gsflnu33B089g03b1
 Method BLASTX
 NCBI GI g2642215
 BLAST score 136
 E value 1.0e-08
 Match length 24
 % identity 100
 NCBI Description (AF030386) NOI protein [Arabidopsis thaliana]

Seq. No. 236547
 Seq. ID uC-gsflnu33B089h12b1
 Method BLASTX
 NCBI GI g3241943
 BLAST score 140
 E value 1.0e-08
 Match length 34
 % identity 76
 NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236548
 Seq. ID uC-gsflnu33B090a07b1
 Method BLASTX
 NCBI GI g3292816
 BLAST score 580
 E value 4.0e-60
 Match length 134
 % identity 33
 NCBI Description (AL031018) putative fizzy-related protein [Arabidopsis thaliana]

Seq. No. 236549
 Seq. ID uC-gsflnu33B090b08b1
 Method BLASTX
 NCBI GI g2129677
 BLAST score 170
 E value 1.0e-12
 Match length 45
 % identity 67
 NCBI Description probable1 N-acetyltransferase hookless 1 - Arabidopsis thaliana >gi_1277090 (U50399) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi_1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi_4468983_emb_CAB38297_ (AL035605) probable N-acetyltransferase hookless 1 [Arabidopsis thaliana]

Seq. No. 236550
 Seq. ID uC-gsflnu33B090b12b1
 Method BLASTX
 NCBI GI g3355468
 BLAST score 150
 E value 3.0e-10

Match length 51
 % identity 67
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 236551
 Seq. ID uC-gsflnu33B090c05b1
 Method BLASTX
 NCBI GI g729506
 BLAST score 530
 E value 3.0e-54
 Match length 110
 % identity 89
 NCBI Description NARINGENIN,2-OXOGLUTARATE 3-DIOXYGENASE (FLAVONONE-3-HYDROXYLASE) (FHT) >gi_481216_pir__S38338 naringenin 3-dioxygenase - common stock >gi_288107_emb_CAA51192_ (X72594) naringenin,2-oxoglutarate 3-dioxygenase [Matthiola incana]

Seq. No. 236552
 Seq. ID uC-gsflnu33B090d05b1
 Method BLASTX
 NCBI GI g2864625
 BLAST score 355
 E value 8.0e-34
 Match length 102
 % identity 67
 NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 236553
 Seq. ID uC-gsflnu33B090d06b1
 Method BLASTX
 NCBI GI g1632822
 BLAST score 245
 E value 3.0e-21
 Match length 75
 % identity 68
 NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi_1667594 (U77297) transmembrane protein [Oryza sativa]

Seq. No. 236554
 Seq. ID uC-gsflnu33B090d10b1
 Method BLASTX
 NCBI GI g531389
 BLAST score 319
 E value 1.0e-29
 Match length 104
 % identity 60
 NCBI Description (U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq. No. 236555
 Seq. ID uC-gsflnu33B090f03b1
 Method BLASTX
 NCBI GI g1773330
 BLAST score 577
 E value 9.0e-60

Seq. ID uC-gsflnu33B090h04b1
 Method BLASTX
 NCBI GI g4389417
 BLAST score 509
 E value 6.0e-52
 Match length 105
 % identity 87
 NCBI Description (AF055369) nitrate reductase [Glycine max]

Seq. No. 236562
 Seq. ID uC-gsflnu33B090h10b1
 Method BLASTX
 NCBI GI g4468990
 BLAST score 138
 E value 7.0e-09
 Match length 53
 % identity 58
 NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 236563
 Seq. ID uC-gsflnu33B090h11b1
 Method BLASTX
 NCBI GI g2760837
 BLAST score 256
 E value 4.0e-22
 Match length 129
 % identity 40
 NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 236564
 Seq. ID uC-gsflnu33B091b03b1
 Method BLASTX
 NCBI GI g2245132
 BLAST score 279
 E value 8.0e-25
 Match length 77
 % identity 70
 NCBI Description (Z97344) syntaxin [Arabidopsis thaliana]

Seq. No. 236565
 Seq. ID uC-gsflnu33B091b11b1
 Method BLASTX
 NCBI GI g3582260
 BLAST score 354
 E value 9.0e-34
 Match length 82
 % identity 84
 NCBI Description (M27221) lysyl-tRNA synthetase [Sinorhizobium meliloti]

Seq. No. 236566
 Seq. ID uC-gsflnu33B091c07b1
 Method BLASTX
 NCBI GI g1345132
 BLAST score 289
 E value 2.0e-26
 Match length 60
 % identity 93

Match length 73
 % identity 62
 NCBI Description (AC006587) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 236572
 Seq. ID uC-gsflnu33B092a06b1
 Method BLASTX
 NCBI GI g602292
 BLAST score 442
 E value 6.0e-44
 Match length 104
 % identity 84
 NCBI Description (U17987) RCH2 protein [Brassica napus]

Seq. No. 236573
 Seq. ID uC-gsflnu33B092b01b1
 Method BLASTX
 NCBI GI g861366
 BLAST score 359
 E value 4.0e-34
 Match length 125
 % identity 57
 NCBI Description (U28991) coded for by C. elegans cDNA cm21c7 [Caenorhabditis elegans]

Seq. No. 236574
 Seq. ID uC-gsflnu33B092b10b1
 Method BLASTX
 NCBI GI g3024127
 BLAST score 369
 E value 1.0e-35
 Match length 91
 % identity 77
 NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
 >gi_1655578_emb_CAA95857_(Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus]

Seq. No. 236575
 Seq. ID uC-gsflnu33B092c08b1
 Method BLASTX
 NCBI GI g549750
 BLAST score 148
 E value 2.0e-09
 Match length 116
 % identity 34
 NCBI Description HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION
 >gi_539221_pir_S38045 hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_(Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No. 236576
 Seq. ID uC-gsflnu33B092e07b1
 Method BLASTX
 NCBI GI g2245132
 BLAST score 153

E value 2.0e-10
Match length 42
% identity 71
NCBI Description (297344) syntaxin [Arabidopsis thaliana]

Seq. No. 236577
Seq. ID uC-gsflnu33B092f11b1
Method BLASTX
NCBI GI g2306917
BLAST score 239
E value 3.0e-36
Match length 85
% identity 93
NCBI Description (AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No. 236578
Seq. ID uC-gsflnu33B092g09b1
Method BLASTX
NCBI GI g3098571
BLAST score 236
E value 9.0e-20
Match length 134
% identity 37
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]

Seq. No. 236579
Seq. ID uC-gsflnu33B093b08b1
Method BLASTX
NCBI GI g3372233
BLAST score 134
E value 3.0e-12
Match length 70
% identity 60
NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana]

Seq. No. 236580
Seq. ID uC-gsflnu33B093b11b1
Method BLASTX
NCBI GI g4467135
BLAST score 395
E value 2.0e-38
Match length 130
% identity 60
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 236581
Seq. ID uC-gsflnu33B093c02b1
Method BLASTX
NCBI GI g2181190
BLAST score 152
E value 5.0e-10
Match length 99
% identity 37
NCBI Description (Y12531) serine/threonine kinase [Brassica oleracea]

Seq. No. 236582
 Seq. ID uC-gsflnu33B093c03b1
 Method BLASTX
 NCBI GI g1076422
 BLAST score 523
 E value 2.0e-53
 Match length 127
 % identity 76
 NCBI Description transcription factor OBF4 - Arabidopsis thaliana
 >gi_414613_emb_CAA49524_(X69899) ocs-element binding
 factor 4 [Arabidopsis thaliana]

Seq. No. 236583
 Seq. ID uC-gsflnu33B093c04b1
 Method BLASTX
 NCBI GI g2924514
 BLAST score 472
 E value 2.0e-47
 Match length 124
 % identity 70
 NCBI Description (AL022023) protein kinase - like [Arabidopsis thaliana]

Seq. No. 236584
 Seq. ID uC-gsflnu33B093c08b1
 Method BLASTX
 NCBI GI g4314359
 BLAST score 334
 E value 2.0e-31
 Match length 102
 % identity 60
 NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236585
 Seq. ID uC-gsflnu33B093c10b1
 Method BLASTX
 NCBI GI g2829899
 BLAST score 147
 E value 3.0e-09
 Match length 65
 % identity 45
 NCBI Description (AC002311) similar to ripening-induced protein,
 gp_AJ001449_2465015 and major#latex protein,
 gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No. 236586
 Seq. ID uC-gsflnu33B093c11b1
 Method BLASTX
 NCBI GI g2144098
 BLAST score 353
 E value 2.0e-33
 Match length 146
 % identity 49
 NCBI Description SC2 - rat >gi_256994 bbs_115268 (S45663) SC2=synaptic
 glycoprotein [rats, brain, Peptide, 308 aa] [Rattus sp.]

Seq. No. 236587
 Seq. ID uC-gsflnu33B093d02b1

Method BLASTX
 NCBI GI g4220472
 BLAST score 394
 E value 3.0e-38
 Match length 122
 % identity 58
 NCBI Description (AC006069) similar to yeast cccl protein [Arabidopsis thaliana]

Seq. No. 236588
 Seq. ID uC-gsflnu33B093d04b1
 Method BLASTX
 NCBI GI g1632831
 BLAST score 333
 E value 5.0e-31
 Match length 72
 % identity 92
 NCBI Description (Z49698) orf [Ricinus communis]

Seq. No. 236589
 Seq. ID uC-gsflnu33B093d10b1
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 1.0e-14
 Match length 47
 % identity 68
 NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No. 236590
 Seq. ID uC-gsflnu33B093e01b1
 Method BLASTX
 NCBI GI g3258570
 BLAST score 297
 E value 7.0e-27
 Match length 143
 % identity 46
 NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

Seq. No. 236591
 Seq. ID uC-gsflnu33B093e08b1
 Method BLASTX
 NCBI GI g3850587
 BLAST score 258
 E value 3.0e-22
 Match length 144
 % identity 40
 NCBI Description (AC005278) Strong similarity to gi_2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No. 236592
 Seq. ID uC-gsflnu33B093f12b1
 Method BLASTX
 NCBI GI g1346172
 BLAST score 284

E value 2.0e-25
 Match length 57
 % identity 91
 NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78)
 (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)
 >gi_170384 (L08830) glucose-regulated protein 78
 [Lycopersicon esculentum]

Seq. No. 236593
 Seq. ID uC-gsflnu33B093g03b1
 Method BLASTX
 NCBI GI g3549681
 BLAST score 391
 E value 6.0e-38
 Match length 134
 % identity 57
 NCBI Description (AL031394) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No. 236594
 Seq. ID uC-gsflnu33B093h09b1
 Method BLASTX
 NCBI GI g1934730
 BLAST score 330
 E value 8.0e-31
 Match length 81
 % identity 79
 NCBI Description (U95036) germin-like protein [Arabidopsis thaliana]

Seq. No. 236595
 Seq. ID uC-gsflnu33B094b01b1
 Method BLASTX
 NCBI GI g3033400
 BLAST score 293
 E value 1.0e-26
 Match length 86
 % identity 66
 NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 236596
 Seq. ID uC-gsflnu33B094b08b1
 Method BLASTX
 NCBI GI g2499015
 BLAST score 173
 E value 2.0e-12
 Match length 102
 % identity 36
 NCBI Description TRIGGER FACTOR (TF) >gi_1001378_dbj_BAA10868_ (D64006)
 trigger factor [Synechocystis sp.]

Seq. No. 236597
 Seq. ID uC-gsflnu33B094c07b1
 Method BLASTX
 NCBI GI g4220474
 BLAST score 252
 E value 9.0e-22

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Match length 117
% identity 50
NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No. 236598
Seq. ID uC-gsflnu33B094c11b1
Method BLASTX
NCBI GI g3819697
BLAST score 197
E value 2.0e-15
Match length 100
% identity 47
NCBI Description (AJ009608) BnMAP4K alpha1 [Brassica napus]

Seq. No. 236599
Seq. ID uC-gsflnu33B094f05b1
Method BLASTX
NCBI GI g4545262
BLAST score 143
E value 2.0e-09
Match length 34
% identity 85
NCBI Description (AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No. 236600
Seq. ID uC-gsflnu33B094g09b1
Method BLASTX
NCBI GI g3236240
BLAST score 179
E value 2.0e-13
Match length 81
% identity 49
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 236601
Seq. ID uC-gsflnu33B094g10b1
Method BLASTX
NCBI GI g3702324
BLAST score 149
E value 1.0e-09
Match length 107
% identity 35
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236602
Seq. ID uC-gsflnu33B094g12b1
Method BLASTX
NCBI GI g2290532
BLAST score 238
E value 3.0e-20
Match length 53
% identity 85
NCBI Description (U94748) AN11 [Petunia x hybrida]

Seq. No. 236603

BLAST score 164
 E value 1.0e-11
 Match length 58
 % identity 55
 NCBI Description (AB009307) bpwl [Hordeum vulgare]

Seq. No. 236609
 Seq. ID uC-gsflnu33B097a12b1
 Method BLASTX
 NCBI GI g1352186
 BLAST score 368
 E value 2.0e-35
 Match length 118
 % identity 58
 NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No. 236610
 Seq. ID uC-gsflnu33B097c08b1
 Method BLASTX
 NCBI GI g1076746
 BLAST score 200
 E value 8.0e-16
 Match length 40
 % identity 93
 NCBI Description heat shock protein 70 - rice (fragment)
 >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No. 236611
 Seq. ID uC-gsflnu33B098b10b1
 Method BLASTX
 NCBI GI g3319882
 BLAST score 303
 E value 3.0e-28
 Match length 65
 % identity 91
 NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No. 236612
 Seq. ID uC-gsflnu33B100b06b1
 Method BLASTX
 NCBI GI g973313
 BLAST score 346
 E value 4.0e-55
 Match length 117
 % identity 93
 NCBI Description (U30250) myo-inositol 1-phosphate synthase isozyme-2 [Arabidopsis thaliana]

Seq. No. 236613
 Seq. ID uC-gsflnu33B100b09b1
 Method BLASTX
 NCBI GI g421826
 BLAST score 431

% identity 57
 NCBI Description (AC002391) putative serine/threonine protein kinase
 [Arabidopsis thaliana]

Seq. No. 236619
 Seq. ID uC-gsflnu33B101b07b1
 Method BLASTX
 NCBI GI g4512263
 BLAST score 520
 E value 4.0e-53
 Match length 128
 % identity 78
 NCBI Description (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]

Seq. No. 236620
 Seq. ID uC-gsflnu33B101c03b1
 Method BLASTX
 NCBI GI g1172995
 BLAST score 268
 E value 2.0e-23
 Match length 107
 % identity 52
 NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir_S52084 ribosomal
 protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
 ribosomal protein L22 [Rattus norvegicus]
 >gi_1093952_prf_2105193A ribosomal protein L22 [Rattus
 norvegicus]

Seq. No. 236621
 Seq. ID uC-gsflnu33B101d03b1
 Method BLASTX
 NCBI GI g544370
 BLAST score 203
 E value 7.0e-16
 Match length 55
 % identity 64
 NCBI Description GAR1 PROTEIN >gi_422064_pir_S33691 GAR1 protein - fission
 yeast (Schizosaccharomyces pombe) >gi_297009_emb_CAA79628_
 (Z19576) snoRNP protein GAR1 [Schizosaccharomyces pombe]
 >gi_1799516_dbj_BAA19143_ (AB000537) snoRNP protein GAR 1
 [Schizosaccharomyces pombe] >gi_2104450_emb_CAB08787_
 (Z95397) Garlp [Schizosaccharomyces pombe]
 >gi_2842463_emb_CAA16841.1_ (AL021747) gar1 protein; small
 nucleolar rnp required for pre-mrna for pre-mrna processing
 [Schizosaccharomyces pombe]

Seq. No. 236622
 Seq. ID uC-gsflnu33B101d11b1
 Method BLASTX
 NCBI GI g3096945
 BLAST score 400
 E value 5.0e-39
 Match length 110
 % identity 73
 NCBI Description (AL023094) putative auxin-regulated protein [Arabidopsis
 thaliana]

Seq. No. 236623
 Seq. ID uC-gsflnu33B101e02b1
 Method BLASTX
 NCBI GI g3128209
 BLAST score 681
 E value 8.0e-72
 Match length 166
 % identity 41
 NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No. 236624
 Seq. ID uC-gsflnu33B101f03b1
 Method BLASTX
 NCBI GI g3023817
 BLAST score 466
 E value 1.0e-46
 Match length 96
 % identity 92
 NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No. 236625
 Seq. ID uC-gsflnu33B101f07b1
 Method BLASTX
 NCBI GI g2136348
 BLAST score 142
 E value 1.0e-08
 Match length 95
 % identity 36
 NCBI Description UDP-galactose transporter related isozyme 3 - human >gi_1669564_dbj_BAA13527_ (D87991) UGTrell [Rattus rattus]

Seq. No. 236626
 Seq. ID uC-gsflnu33B101f08b1
 Method BLASTX
 NCBI GI g4454471
 BLAST score 190
 E value 2.0e-14
 Match length 107
 % identity 42
 NCBI Description (AC006234) putative G protein coupled receptor [Arabidopsis thaliana]

Seq. No. 236627
 Seq. ID uC-gsflnu33B101h07b1
 Method BLASTX
 NCBI GI g464980
 BLAST score 401
 E value 4.0e-39
 Match length 76
 % identity 93
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_166422 (L06967) ubiquitin carrier protein [Medicago sativa]

Seq. No. 236628

% identity 72
 NCBI Description (AC006413) putative 12-oxophytodienoate-10,11-reductase
 [Arabidopsis thaliana]

Seq. No. 236634
 Seq. ID uC-gsflnu33B107h02b1
 Method BLASTX
 NCBI GI g3935174
 BLAST score 182
 E value 2.0e-13
 Match length 131
 % identity 37
 NCBI Description (AC004557) F17L21.17 [Arabidopsis thaliana]

Seq. No. 236635
 Seq. ID uC-gsflnu33B107h03b1
 Method BLASTX
 NCBI GI g4544462
 BLAST score 555
 E value 4.0e-57
 Match length 140
 % identity 75
 NCBI Description (AC006580) putative NAM protein [Arabidopsis thaliana]

Seq. No. 236636
 Seq. ID uC-gsflnu33B107h05b1
 Method BLASTX
 NCBI GI g4406815
 BLAST score 490
 E value 2.0e-49
 Match length 156
 % identity 65
 NCBI Description (AC006201) putative peptide methionine sulfoxide reductase
 [Arabidopsis thaliana]

Seq. No. 236637
 Seq. ID uC-gsflnu33B107h11b1
 Method BLASTX
 NCBI GI g2959781
 BLAST score 650
 E value 3.0e-68
 Match length 157
 % identity 78
 NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 236638
 Seq. ID uC-gsflnu33B108a12b1
 Method BLASTX
 NCBI GI g4325369
 BLAST score 152
 E value 3.0e-10
 Match length 47
 % identity 60
 NCBI Description (AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No. 236639
 Seq. ID uC-gsflnu33B108b08b1

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Seq. No.          236641
Seq. ID           uC-gsflnu33B108d01b1
Method            BLASTX
NCBI GI           g1363484
BLAST score       341
E value           5.0e-32
Match length      103
% identity        66
NCBI Description  IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415)
                  IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin
                  inducible protein, IAA13 [Arabidopsis thaliana]
```

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Seq. No.          236643
Seq. ID           uC-gsflnu33B108e08b1
Method            BLASTX
NCBI GI           g3334244
BLAST score       380
E value           1.0e-36
Match length      88
% identity        80
NCBI Description   LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
                  (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                  MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                  >gi_2113825_emb_CAA73691_ (Y13239) Glyoxalase I [Brassica
                  juncea]
```

34317

NCBI GI g2262118
 BLAST score 140
 E value 5.0e-09
 Match length 35
 % identity 80
 NCBI Description (AC002343) cell division protein isolog [Arabidopsis thaliana]

Seq. No. 236645
 Seq. ID uC-gsflnu33B108f04b1
 Method BLASTX
 NCBI GI g2505870
 BLAST score 156
 E value 3.0e-10
 Match length 48
 % identity 56
 NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236646
 Seq. ID uC-gsflnu33B108g11b1
 Method BLASTX
 NCBI GI g2827715
 BLAST score 468
 E value 5.0e-47
 Match length 129
 % identity 69
 NCBI Description (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 236647
 Seq. ID uC-gsflnu33B108h04b1
 Method BLASTX
 NCBI GI g2244835
 BLAST score 283
 E value 3.0e-25
 Match length 91
 % identity 62
 NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 236648
 Seq. ID uC-gsflnu33B109a02b1
 Method BLASTX
 NCBI GI g4006829
 BLAST score 459
 E value 9.0e-46
 Match length 168
 % identity 55
 NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 236649
 Seq. ID uC-gsflnu33B109b02b1
 Method BLASTX
 NCBI GI g3135274
 BLAST score 196
 E value 3.0e-15
 Match length 76
 % identity 53

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NCBI Description	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]
Seq. No.	236650
Seq. ID	uC-gsflnu33B109d01b1
Method	BLASTX
NCBI GI	g3738283
BLAST score	402
E value	3.0e-39
Match length	82
% identity	85
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	236651
Seq. ID	uC-gsflnu33B109d04b1
Method	BLASTX
NCBI GI	g3461817
BLAST score	178
E value	6.0e-13
Match length	64
% identity	56
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.	236652
Seq. ID	uC-gsflnu33B109e02b1
Method	BLASTX
NCBI GI	g3785999
BLAST score	349
E value	6.0e-33
Match length	91
% identity	73
NCBI Description	(AC005499) putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]
Seq. No.	236653
Seq. ID	uC-gsflnu33B109f02b1
Method	BLASTX
NCBI GI	g4006914
BLAST score	246
E value	8.0e-21
Match length	72
% identity	71
NCBI Description	(Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]
Seq. No.	236654
Seq. ID	uC-gsflnu33B109f03b1
Method	BLASTX
NCBI GI	g1173043
BLAST score	308
E value	4.0e-28
Match length	65
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_479441_pir_S33899.ribosomal protein L38 - tomato (cv. MoneyMaker) >gi_313027_emb_CAA49599_(X69979) ribosomal protein L38 [Lycopersicon esculentum]

BLAST score 220
 E value 3.0e-18
 Match length 60
 % identity 73
 NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236666
 Seq. ID uC-gsflnu33B111d04b1
 Method BLASTX
 NCBI GI g4432821
 BLAST score 196
 E value 6.0e-15
 Match length 123
 % identity 39
 NCBI Description (AC006593) putative transmembrane protein [Arabidopsis thaliana]

Seq. No. 236667
 Seq. ID uC-gsflnu33B111d08b1
 Method BLASTX
 NCBI GI g113116
 BLAST score 573
 E value 4.0e-59
 Match length 175
 % identity 60
 NCBI Description ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
 >gi_111396_pir_A35007 ATP citrate (pro-S)-lyase (EC
 4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase
 [Rattus norvegicus]

Seq. No. 236668
 Seq. ID uC-gsflnu33B111e08b1
 Method BLASTX
 NCBI GI g3236259
 BLAST score 736
 E value 3.0e-78
 Match length 163
 % identity 82
 NCBI Description (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 236669
 Seq. ID uC-gsflnu33B111e12b1
 Method BLASTX
 NCBI GI g4049347
 BLAST score 418
 E value 6.0e-41
 Match length 169
 % identity 50
 NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 236670
 Seq. ID uC-gsflnu33B111g03b1
 Method BLASTX
 NCBI GI g3024491
 BLAST score 206
 E value 4.0e-16

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BLAST score 244
E value 1.0e-20
Match length 110
% identity 52
NCBI Description (AJ010463) RNA helicase [Arabidopsis thaliana]

Seq. No. 236708
Seq. ID uC-gsflnu33B115e09b1
Method BLASTX
NCBI GI g4219092
BLAST score 277
E value 2.0e-24
Match length 75
% identity 72
NCBI Description (AF117707) putative copper/zinc superoxide dismutase copper chaperone precursor [Lycopersicon esculentum]

Seq. No. 236709
Seq. ID uC-gsflnu33B115e11b1
Method BLASTX
NCBI GI g1076291
BLAST score 378
E value 1.0e-36
Match length 95
% identity 75
NCBI Description amino acid transporter AAT1 - Arabidopsis thaliana
>gi_2911069_emb_CAA17531_ (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]

Seq. No. 236710
Seq. ID uC-gsflnu33B115f02b1
Method BLASTX
NCBI GI g2832629
BLAST score 182
E value 2.0e-13
Match length 87
% identity 45
NCBI Description (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No. 236711
Seq. ID uC-gsflnu33B115f08b1
Method BLASTX
NCBI GI g3241945
BLAST score 269
E value 9.0e-24
Match length 76
% identity 57
NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]

Seq. No. 236712
Seq. ID uC-gsflnu33B115g02b1
Method BLASTX
NCBI GI g3335378
BLAST score 303
E value 1.0e-27
Match length 72

Method BLASTX
 NCBI GI g4539314
 BLAST score 194
 E value 2.0e-15
 Match length 59
 % identity 64
 NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 236719
 Seq. ID uC-gsflnu33B126b08b1
 Method BLASTX
 NCBI GI g629602
 BLAST score 243
 E value 8.0e-31
 Match length 90
 % identity 76
 NCBI Description probable imbibition protein - wild cabbage
 >gi_488787_emb_CAA55893_(X79330) putative imbibition
 protein [Brassica oleracea]

Seq. No. 236720
 Seq. ID uC-gsflnu33B126f12b1
 Method BLASTX
 NCBI GI g2673914
 BLAST score 314
 E value 8.0e-29
 Match length 154
 % identity 49
 NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236721
 Seq. ID uC-gsflnu33B126g11b1
 Method BLASTX
 NCBI GI g1778376
 BLAST score 604
 E value 7.0e-63
 Match length 148
 % identity 78
 NCBI Description (U81288) PsRT17-1 [Pisum sativum]

Seq. No. 236722
 Seq. ID uC-gsflnu33B126h04b1
 Method BLASTX
 NCBI GI g3831467
 BLAST score 161
 E value 3.0e-11
 Match length 78
 % identity 40
 NCBI Description (AC005700) putative beta-amylase [Arabidopsis thaliana]

Seq. No. 236723
 Seq. ID uC-gsflnu33B126h10b1
 Method BLASTX
 NCBI GI g1769907
 BLAST score 142
 E value 1.0e-08
 Match length 32


```
% identity      69
NCBI Description (X92975) xyloglucan endo-transglycosylase [Arabidopsis
                  thaliana]
```

```
Seq. No.          236724
Seq. ID           uC-gsflnu33B127b02b1
Method            BLASTX
NCBI GI           g2501449
BLAST score       216
E value           4.0e-20
Match length      61
% identity        90
```

NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi_1668773_emb_CAA67922_ (X99608) ubiquitin-like protein [Oryza sativa]

```
Seq. No.          236725
Seq. ID           uC-gsflnu33B127b06b1
Method            BLASTX
NCBI GI           g1402916
BLAST score       192
E value           1.0e-14
Match length      66
% identity        64
```

NCBI Description (X98319) peroxidase [Arabidopsis thaliana]
>gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a
[Arabidopsis thaliana]

```
Seq. No.      236726
Seq. ID      uC-gsflnu33B127b08b1
Method      BLASTX
NCBI GI      g1771780
BLAST score   315
E value      6.0e-29
Match length  57
% identity    98
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]
```

```
Seq. No.      236727
Seq. ID       uC-gsflnu33B127c04b1
Method        BLASTX
NCBI GI       g2160322
BLAST score    201
E value       8.0e-16
Match length   58
% identity     66
NCBI Description (D16139) cytokinin binding protein CBP57 [Nicotiana
                sylvestris]
```

```
Seq. No.      236728
Seq. ID       uC-gsflnu33B127c07b1
Method        BLASTX
NCBI GI       g548852
BLAST score    171
E value        2.0e-12
Match length   40
% identity     80
NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal
```


protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
subunit ribosomal protein [Oryza sativa]

Seq. No. 236729
Seq. ID uC-gsflnu33B127c10b1
Method BLASTX
NCBI GI g3122572
BLAST score 739
E value 1.0e-78
Match length 143
% identity 97
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
SUBUNIT) >gi_1084434_pir_S52737 NADH dehydrogenase
(ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
>gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
complex I subunit [Solanum tuberosum]

Seq. No. 236730
Seq. ID uC-gsflnu33B127g02b1
Method BLASTX
NCBI GI g2213584
BLAST score 338
E value 8.0e-32
Match length 120
% identity 58
NCBI Description (AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No. 236731
Seq. ID uC-gsflnu33B127g11b1
Method BLASTX
NCBI GI g4539010
BLAST score 143
E value 7.0e-09
Match length 131
% identity 39
NCBI Description (AL049481) putative DNA-directed RNA polymerase
[Arabidopsis thaliana]

Seq. No. 236732
Seq. ID uC-gsflnu33B128b07b1
Method BLASTX
NCBI GI g2342676
BLAST score 568
E value 1.0e-58
Match length 129
% identity 81
NCBI Description (AC000106) Strong similarity to Oryza NADPH oxidase
(gb_X93301). [Arabidopsis thaliana]

Seq. No. 236733
Seq. ID uC-gsflnu33B128c04b1
Method BLASTX
NCBI GI g3395431
BLAST score 378
E value 2.0e-36
Match length 85

% identity 84
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

 Seq. No. 236734
 Seq. ID uC-gsflnu33B128c06b1
 Method BLASTX
 NCBI GI g3033375
 BLAST score 305
 E value 7.0e-28
 Match length 128
 % identity 48
 NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

 Seq. No. 236735
 Seq. ID uC-gsflnu33B128d02b1
 Method BLASTX
 NCBI GI g3834322
 BLAST score 268
 E value 1.0e-23
 Match length 87
 % identity 61
 NCBI Description (AC005679) EST gb_R30300 comes from this gene. [Arabidopsis thaliana]

 Seq. No. 236736
 Seq. ID uC-gsflnu33B128d11b1
 Method BLASTX
 NCBI GI g2832304
 BLAST score 347
 E value 6.0e-33
 Match length 115
 % identity 60
 NCBI Description (AF044489) receptor-like protein kinase [Oryza sativa]

 Seq. No. 236737
 Seq. ID uC-gsflnu33B128e11b1
 Method BLASTX
 NCBI GI g2129921
 BLAST score 178
 E value 4.0e-13
 Match length 35
 % identity 94
 NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

 Seq. No. 236738
 Seq. ID uC-gsflnu33B128f02b1
 Method BLASTX
 NCBI GI g4098246
 BLAST score 356
 E value 6.0e-34
 Match length 116
 % identity 63
 NCBI Description (U76410) homeobox 2 protein [Lycopersicon esculentum]

 Seq. No. 236739

Seq. ID uC-gsflnu33B128f10b1
 Method BLASTX
 NCBI GI g3236241
 BLAST score 371
 E value 1.0e-35
 Match length 100
 % identity 66
 NCBI Description (AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 236740
 Seq. ID uC-gsflnu33B128g10b1
 Method BLASTX
 NCBI GI g1168470
 BLAST score 239
 E value 4.0e-20
 Match length 109
 % identity 54
 NCBI Description PROTEIN KINASE APK1A >gi_282877_pir_S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No. 236741
 Seq. ID uC-gsflnu33B129d05b1
 Method BLASTX
 NCBI GI g4115383
 BLAST score 284
 E value 2.0e-25
 Match length 119
 % identity 18
 NCBI Description (AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 236742
 Seq. ID uC-gsflnu33B129e01b1
 Method BLASTX
 NCBI GI g2062172
 BLAST score 379
 E value 9.0e-37
 Match length 82
 % identity 83
 NCBI Description (AC001645) unknown protein [Arabidopsis thaliana]

Seq. No. 236743
 Seq. ID uC-gsflnu33B129e04b1
 Method BLASTX
 NCBI GI g2935298
 BLAST score 472
 E value 2.0e-47
 Match length 97
 % identity 97
 NCBI Description (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No. 236744

Seq. ID uC-gsflnu33B130a03b1
 Method BLASTX
 NCBI GI g3746060
 BLAST score 235
 E value 1.0e-19
 Match length 59
 % identity 68
 NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 236745
 Seq. ID uC-gsflnu33B130a07b1
 Method BLASTX
 NCBI GI g2920706
 BLAST score 231
 E value 4.0e-19
 Match length 97
 % identity 46
 NCBI Description (Y13568) beta-xylosidase [Emmericella nidulans]

Seq. No. 236746
 Seq. ID uC-gsflnu33B130b04b1
 Method BLASTX
 NCBI GI g231660
 BLAST score 341
 E value 4.0e-32
 Match length 131
 % identity 62
 NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No. 236747
 Seq. ID uC-gsflnu33B130d08b1
 Method BLASTX
 NCBI GI g125393
 BLAST score 176
 E value 7.0e-13
 Match length 101
 % identity 39
 NCBI Description HOMOSERINE KINASE (HK) >gi_79795_pir_S03743 homoserine kinase (EC 2.7.1.39) - Calothrix sp. >gi_43396_emb_CAA68576_ (Y00522) homoserine kinase (AA 1-307) [Calothrix PCC7601]

Seq. No. 236748
 Seq. ID uC-gsflnu33B130f05b1
 Method BLASTX
 NCBI GI g1705930
 BLAST score 312
 E value 1.0e-28
 Match length 93
 % identity 68
 NCBI Description ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1 (ENDOPEPTIDASE CLP 1) >gi_1001349_dbj_BAA10836_ (D64006) ATP-dependent protease ClpP [Synechocystis sp.]

Seq. No. 236749
 Seq. ID uC-gsflnu33B130h09b1
 Method BLASTX
 NCBI GI g4234955

09684015-101000

GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
[Arabidopsis thaliana]

Seq. No.	236755
Seq. ID	uC-gsflnu33B131f03b1
Method	BLASTX
NCBI GI	g3005931
BLAST score	398
E value	9.0e-39
Match length	129
% identity	42
NCBI Description	(AJ005016) ABC transporter [Homo sapiens]
Seq. No.	236756
Seq. ID	uC-gsflnu33B131f10b1
Method	BLASTX
NCBI GI	g3046995
BLAST score	178
E value	3.0e-13
Match length	86
% identity	44
NCBI Description	(AF056717) ash212 [Homo sapiens]
Seq. No.	236757
Seq. ID	uC-gsflnu33B131h02b1
Method	BLASTX
NCBI GI	g1621463
BLAST score	250
E value	9.0e-22
Match length	49
% identity	88
NCBI Description	(U73104) laccase [Liriodendron tulipifera]
Seq. No.	236758
Seq. ID	uC-gsflnu33B131h10b1
Method	BLASTX
NCBI GI	g2462748
BLAST score	137
E value	9.0e-09
Match length	27
% identity	100
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]
Seq. No.	236759
Seq. ID	uC-gsflnu33B132e12b1
Method	BLASTX
NCBI GI	g139799
BLAST score	266
E value	2.0e-23
Match length	102
% identity	53
NCBI Description	XANTHINE DEHYDROGENASE (XD) (ROSY LOCUS PROTEIN) >gi_8831_emb_CAA68409_ (Y00308) xanthine dehydrogenase [Drosophila melanogaster]
Seq. No.	236760

Seq. ID uC-gsflnu33B132g01b1
 Method BLASTX
 NCBI GI g2673912
 BLAST score 167
 E value 9.0e-12
 Match length 46
 % identity 74
 NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]

Seq. No. 236761
 Seq. ID uC-gsflnu33B132h10b1
 Method BLASTX
 NCBI GI g4454051
 BLAST score 572
 E value 4.0e-59
 Match length 139
 % identity 76
 NCBI Description (AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 236762
 Seq. ID uC-gsflnu33B132h12b1
 Method BLASTX
 NCBI GI g4544427
 BLAST score 286
 E value 2.0e-25
 Match length 76
 % identity 82
 NCBI Description (AC006955) putative ferredoxin-thioredoxin reductase [Arabidopsis thaliana]

Seq. No. 236763
 Seq. ID uC-gsflnu33B133b03b1
 Method BLASTX
 NCBI GI g2827715
 BLAST score 280
 E value 2.0e-25
 Match length 71
 % identity 77
 NCBI Description (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 236764
 Seq. ID uC-gsflnu33B133b07b1
 Method BLASTX
 NCBI GI g1498338
 BLAST score 366
 E value 3.0e-35
 Match length 79
 % identity 95
 NCBI Description (U60502) actin [Glycine max]

Seq. No. 236765
 Seq. ID uC-gsflnu33B133f12b1
 Method BLASTX
 NCBI GI g129590
 BLAST score 567

E value 9.0e-59
 Match length 116
 % identity 94
 NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_99990_pir_S17444
 phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - alfalfa
 >gi_19650_emb_CAA41169_ (X58180) phenylalanine
 ammonia-lyase [Medicago sativa]

Seq. No. 236766
 Seq. ID uC-gsflnu33B133h09b1
 Method BLASTX
 NCBI GI g422029
 BLAST score 292
 E value 2.0e-26
 Match length 66
 % identity 77
 NCBI Description transcription factor OBF3.2, ocs element-binding - maize
 >gi_297018_emb_CAA48904_ (X69152) ocs-element binding
 factor 3.2 [Zea mays]

Seq. No. 236767
 Seq. ID uC-gsflnu33B134b08b1
 Method BLASTX
 NCBI GI g3242789
 BLAST score 515
 E value 2.0e-52
 Match length 136
 % identity 76
 NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis
 thaliana]

Seq. No. 236768
 Seq. ID uC-gsflnu33B134b12b1
 Method BLASTX
 NCBI GI g2244835
 BLAST score 261
 E value 7.0e-23
 Match length 80
 % identity 64
 NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 236769
 Seq. ID uC-gsflnu33B134c10b1
 Method BLASTX
 NCBI GI g4388727
 BLAST score 226
 E value 9.0e-19
 Match length 76
 % identity 61
 NCBI Description (AC006413) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236770
 Seq. ID uC-gsflnu33B135a10b1
 Method BLASTX
 NCBI GI g1174592
 BLAST score 343
 E value 8.0e-53

NCBI GI g2288988
 BLAST score 231
 E value 3.0e-19
 Match length 113
 % identity 41
 NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236776
 Seq. ID uC-gsflnu33B136c12b1
 Method BLASTX
 NCBI GI g4490303
 BLAST score 410
 E value 4.0e-40
 Match length 99
 % identity 77
 NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 236777
 Seq. ID uC-gsflnu33B136d07b1
 Method BLASTX
 NCBI GI g3763933
 BLAST score 192
 E value 4.0e-15
 Match length 67
 % identity 76
 NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 236778
 Seq. ID uC-gsflnu33B136e02b1
 Method BLASTX
 NCBI GI g135392
 BLAST score 153
 E value 3.0e-10
 Match length 46
 % identity 63
 NCBI Description TUBULIN ALPHA-1 CHAIN >gi_101808_pir_S13336 tubulin
 alpha-1 chain - Emericella nidulans

Seq. No. 236779
 Seq. ID uC-gsflnu33B136e04b1
 Method BLASTX
 NCBI GI g2982268
 BLAST score 280
 E value 4.0e-25
 Match length 57
 % identity 93
 NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea
 mariana]

Seq. No. 236780
 Seq. ID uC-gsflnu33B136g01b1
 Method BLASTX
 NCBI GI g3980377
 BLAST score 416
 E value 7.0e-41
 Match length 140
 % identity 61

Method BLASTX
 NCBI GI g1174595
 BLAST score 416
 E value 6.0e-41
 Match length 105
 % identity 56
 NCBI Description TUBULIN BETA-1 CHAIN >gi_1076658_pir_S50747 beta-tubulin -
 potato >gi_609268_emb_CAA83847_ (Z33382) beta-tubulin
 [Solanum tuberosum]

Seq. No. 236787
 Seq. ID uC-gsflnu33B137f01b1
 Method BLASTX
 NCBI GI g3915737
 BLAST score 255
 E value 4.0e-22
 Match length 57
 % identity 89
 NCBI Description IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP
 ALPHA) >gi_3228370 (AF017252) importin alpha [Lycopersicon
 esculentum]

Seq. No. 236788
 Seq. ID uC-gsflnu33B137g12b1
 Method BLASTX
 NCBI GI g3451074
 BLAST score 592
 E value 2.0e-61
 Match length 135
 % identity 76
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 236789
 Seq. ID uC-gsflnu33B137h11b1
 Method BLASTX
 NCBI GI g2252841
 BLAST score 176
 E value 2.0e-16
 Match length 81
 % identity 57
 NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 236790
 Seq. ID uC-gsflnu33B138a09b1
 Method BLASTX
 NCBI GI g1495366
 BLAST score 234
 E value 1.0e-19
 Match length 134
 % identity 41
 NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 236791
 Seq. ID uC-gsflnu33B138b07b1
 Method BLASTX
 NCBI GI g4455364
 BLAST score 174

E value 1.0e-12
 Match length 42
 % identity 79
 NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No. 236792
 Seq. ID uC-gsflnu33B138b10b1
 Method BLASTX
 NCBI GI g2827528
 BLAST score 473
 E value 2.0e-47
 Match length 132
 % identity 69
 NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 236793
 Seq. ID uC-gsflnu33B138c10b1
 Method BLASTX
 NCBI GI g1871192
 BLAST score 612
 E value 8.0e-64
 Match length 127
 % identity 81
 NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 236794
 Seq. ID uC-gsflnu33B138c12b1
 Method BLASTX
 NCBI GI g1279600
 BLAST score 433
 E value 5.0e-43
 Match length 104
 % identity 77
 NCBI Description (Z71753) pectin methylesterase [Nicotiana plumbaginifolia]

Seq. No. 236795
 Seq. ID uC-gsflnu33B138d11b1
 Method BLASTX
 NCBI GI g4510368
 BLAST score 331
 E value 2.0e-31
 Match length 138
 % identity 61
 NCBI Description (AC007017) putative transcription factor E2F5 [Arabidopsis thaliana]

Seq. No. 236796
 Seq. ID uC-gsflnu33B138f12b1
 Method BLASTX
 NCBI GI g3860256
 BLAST score 177
 E value 7.0e-13
 Match length 70
 % identity 54
 NCBI Description (AC005824) putative tRNA isopentenylpyrophosphate

09634016 101000

thaliana]

Seq. No. 236802
 Seq. ID uC-gsflnu33B140a09b1
 Method BLASTX
 NCBI GI g464981
 BLAST score 683
 E value 4.0e-72
 Match length 142
 % identity 87
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 236803
 Seq. ID uC-gsflnu33B140b01b1
 Method BLASTX
 NCBI GI g2443886
 BLAST score 383
 E value 4.0e-37
 Match length 91
 % identity 81
 NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 236804
 Seq. ID uC-gsflnu33B140b06b1
 Method BLASTX
 NCBI GI g3510254
 BLAST score 494
 E value 5.0e-50
 Match length 108
 % identity 88
 NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 236805
 Seq. ID uC-gsflnu33B140c01b1
 Method BLASTX
 NCBI GI g1771780
 BLAST score 430
 E value 2.0e-42
 Match length 106
 % identity 78
 NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 236806
 Seq. ID uC-gsflnu33B140d06b1
 Method BLASTX
 NCBI GI g3236241
 BLAST score 365
 E value 7.0e-35
 Match length 103
 % identity 71
 NCBI Description (AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 236807
 Seq. ID uC-gsflnu33B140d10b1

E value 1.0e-19
 Match length 133
 % identity 36
 NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No. 236813
 Seq. ID uC-gsflnu33B141d09b1
 Method BLASTX
 NCBI GI g1709692
 BLAST score 461
 E value 3.0e-46
 Match length 101
 % identity 84
 NCBI Description PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O) REDUCTASE) (FRUIT-RIPENING PROTEIN E4)
 >gi_100204_pir_JQ0988 DNA-binding E4 protein - Tomato

Seq. No. 236814
 Seq. ID uC-gsflnu33B141d12b1
 Method BLASTX
 NCBI GI g2921323
 BLAST score 383
 E value 7.0e-37
 Match length 139
 % identity 56
 NCBI Description (AF034112) beta-1,3-glucanase 7 [Glycine max]

Seq. No. 236815
 Seq. ID uC-gsflnu33B141h04b1
 Method BLASTX
 NCBI GI g3169719
 BLAST score 255
 E value 2.0e-22
 Match length 80
 % identity 66
 NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]

Seq. No. 236816
 Seq. ID uC-gsflnu33B142b04b1
 Method BLASTX
 NCBI GI g2632105
 BLAST score 144
 E value 5.0e-09
 Match length 55
 % identity 58
 NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
 >gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 236817
 Seq. ID uC-gsflnu33B142g02b1
 Method BLASTX
 NCBI GI g2702279
 BLAST score 283
 E value 7.0e-26
 Match length 69

BLAST score 362
 E value 2.0e-34
 Match length 141
 % identity 50
 NCBI Description (D90913) PET112 [Synechocystis sp.]

Seq. No. 236823
 Seq. ID uC-gsflnu33B143e09b1
 Method BLASTX
 NCBI GI g1706263
 BLAST score 322
 E value 7.0e-30
 Match length 129
 % identity 48
 NCBI Description CYSTEINE PROTEINASE 5 PRECURSOR >gi_1222694 (L36205) CP5 [Dictyostelium discoideum]

Seq. No. 236824
 Seq. ID uC-gsflnu33B143f02b1
 Method BLASTX
 NCBI GI g1076809
 BLAST score 459
 E value 5.0e-46
 Match length 125
 % identity 78
 NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase [Zea mays]

Seq. No. 236825
 Seq. ID uC-gsflnu33B143f06b1
 Method BLASTX
 NCBI GI g4426964
 BLAST score 331
 E value 6.0e-31
 Match length 80
 % identity 71
 NCBI Description (AF126255) purple acid phosphatase precursor [Anchusa officinalis]

Seq. No. 236826
 Seq. ID uC-gsflnu33B143g12b1
 Method BLASTX
 NCBI GI g4249384
 BLAST score 241
 E value 3.0e-20
 Match length 99
 % identity 44
 NCBI Description (AC005966) Similar to gi_4056506 F3G5.25 nodulin-like protein from Arabidopsis thaliana BAC gb_AC005896. [Arabidopsis thaliana]

Seq. No. 236827
 Seq. ID uC-gsflnu33B143h10b1
 Method BLASTX
 NCBI GI g1172977
 BLAST score 562

NCBI Description immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406
(U52046) immunophilin [Arabidopsis thaliana]

Seq. No. 236843
Seq. ID uC-gsflnu33B145c05b1
Method BLASTX
NCBI GI g3643603
BLAST score 460
E value 4.0e-46
Match length 126
% identity 73
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 236844
Seq. ID uC-gsflnu33B145d02b1
Method BLASTX
NCBI GI g2723477
BLAST score 617
E value 2.0e-64
Match length 149
% identity 80
NCBI Description (D89824) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 236845
Seq. ID uC-gsflnu33B145e04b1
Method BLASTX
NCBI GI g4455202
BLAST score 458
E value 1.0e-45
Match length 146
% identity 60
NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 236846
Seq. ID uC-gsflnu33B145e06b1
Method BLASTX
NCBI GI g1172597
BLAST score 226
E value 1.0e-18
Match length 47
% identity 91
NCBI Description WOUND-INDUCED BASIC PROTEIN >gi_81888_pir_JS0731
wound-inducible basic protein - kidney bean >gi_169365
(L00625) basic protein [Phaseolus vulgaris]
>gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein
[Phaseolus vulgaris]

Seq. No. 236847
Seq. ID uC-gsflnu33B145e10b1
Method BLASTX
NCBI GI g2662415
BLAST score 173
E value 2.0e-12
Match length 56
% identity 54
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No. 236848
 Seq. ID uC-gsflnu33B145f01b1
 Method BLASTX
 NCBI GI g3980384
 BLAST score 351
 E value 3.0e-33
 Match length 109
 % identity 61
 NCBI Description (AC004561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236849
 Seq. ID uC-gsflnu33B145f06b1
 Method BLASTX
 NCBI GI g21309
 BLAST score 341
 E value 4.0e-32
 Match length 81
 % identity 42
 NCBI Description (X57955) 28kD RNA binding protein [Spinacia oleracea]

Seq. No. 236850
 Seq. ID uC-gsflnu33B145g05b1
 Method BLASTX
 NCBI GI g3152560
 BLAST score 176
 E value 8.0e-13
 Match length 65
 % identity 51
 NCBI Description (AC002986) Strong similarity to ser/thr protein kinases, especially gb_X97980 from solanum berthaultii, gb_X90990 from solanum tuberosum and gb_D10909 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 236851
 Seq. ID uC-gsflnu33B145g06b1
 Method BLASTX
 NCBI GI g21309
 BLAST score 346
 E value 1.0e-32
 Match length 79
 % identity 43
 NCBI Description (X57955) 28kD RNA binding protein [Spinacia oleracea]

Seq. No. 236852
 Seq. ID uC-gsflnu33B145h10b1
 Method BLASTX
 NCBI GI g1223579
 BLAST score 215
 E value 2.0e-17
 Match length 108
 % identity 52
 NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 236853
 Seq. ID uC-gsflnu33B146a01b1
 Method BLASTX
 NCBI GI g4559327

Method BLASTX
 NCBI GI g2288999
 BLAST score 153
 E value 5.0e-10
 Match length 127
 % identity 46
 NCBI Description (AC002335) electron transfer flavoprotein ubiquinone
 oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 236859
 Seq. ID uC-gsflnu33B146f12b1
 Method BLASTX
 NCBI GI g3641647
 BLAST score 447
 E value 1.0e-44
 Match length 101
 % identity 78
 NCBI Description (AB006804) ACC synthase [Cucumis sativus]

Seq. No. 236860
 Seq. ID uC-gsflnu33B146g01b1
 Method BLASTX
 NCBI GI g4240253
 BLAST score 141
 E value 6.0e-09
 Match length 75
 % identity 41
 NCBI Description (AB020689) KIAA0882 protein [Homo sapiens]

Seq. No. 236861
 Seq. ID uC-gsflnu33B146g04b1
 Method BLASTX
 NCBI GI g4115913
 BLAST score 508
 E value 1.0e-51
 Match length 152
 % identity 61
 NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of
 oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88,
 N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_
 (AL049524) putative flavanone 3-beta-hydroxylase
 [Arabidopsis thaliana]

Seq. No. 236862
 Seq. ID uC-gsronu33B001a07b1
 Method BLASTX
 NCBI GI g4106696
 BLAST score 262
 E value 9.0e-23
 Match length 68
 % identity 72
 NCBI Description (AB021872) ribosome-sedimenting protein [Pisum sativum]

Seq. No. 236863
 Seq. ID uC-gsronu33B001a09b1
 Method BLASTX
 NCBI GI g1850546

BLAST score 241
 E value 3.0e-20
 Match length 61
 % identity 74
 NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No. 236864
 Seq. ID uC-gsronu33B001c02b1
 Method BLASTX
 NCBI GI g4220469
 BLAST score 145
 E value 5.0e-09
 Match length 51
 % identity 63
 NCBI Description (AC006069) putative receptor protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No. 236865
 Seq. ID uC-gsronu33B001c04b1
 Method BLASTX
 NCBI GI g136057
 BLAST score 510
 E value 7.0e-52
 Match length 130
 % identity 75
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 >gi_99499_pir_A32187 (S)-tetrahydroberberine oxidase -
 Coptis japonica >gi_556171 (J04121) triosephosphate
 isomerase [Coptis japonica]

Seq. No. 236866
 Seq. ID uC-gsronu33B001c10b1
 Method BLASTX
 NCBI GI g1907076
 BLAST score 378
 E value 2.0e-36
 Match length 118
 % identity 60
 NCBI Description (Y07867) pirin [Homo sapiens] >gi_1907078_emb_CAA69195_
 (Y07868) pirin [Homo sapiens]
 >gi_4505823_ref_NP_003653.1_pPIR_pirin

Seq. No. 236867
 Seq. ID uC-gsronu33B001f03b1
 Method BLASTX
 NCBI GI g2979549
 BLAST score 376
 E value 4.0e-36
 Match length 128
 % identity 52
 NCBI Description (AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No. 236868
 Seq. ID uC-gsronu33B001g03b1
 Method BLASTX

NCBI Description (AB010991) 3b-hydroxylase [*Lycopersicon esculentum*]

Seq. No. 236879
 Seq. ID uC-gsronu33B002h05b1
 Method BLASTX
 NCBI GI g2244855
 BLAST score 198
 E value 2.0e-15
 Match length 97
 % identity 45
 NCBI Description (Z97337) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 236880
 Seq. ID uC-gsronu33B004a01b1
 Method BLASTX
 NCBI GI g2262111
 BLAST score 234
 E value 5.0e-24
 Match length 81
 % identity 65
 NCBI Description (AC002343) ribitol dehydrogenase isolog [*Arabidopsis thaliana*]

Seq. No. 236881
 Seq. ID uC-gsronu33B004a06b1
 Method BLASTX
 NCBI GI g3377850
 BLAST score 147
 E value 8.0e-10
 Match length 39
 % identity 77
 NCBI Description (AF076274) contains similarity to *Canis familiaris* signal peptidase complex 25 kDa subunit (GB:U12687) [*Arabidopsis thaliana*]

Seq. No. 236882
 Seq. ID uC-gsronu33B004a08b1
 Method BLASTX
 NCBI GI g4522005
 BLAST score 167
 E value 1.0e-11
 Match length 86
 % identity 41
 NCBI Description (AC007069) putative reverse transcriptase [*Arabidopsis thaliana*]

Seq. No. 236883
 Seq. ID uC-gsronu33B004b02b1
 Method BLASTX
 NCBI GI g3242710
 BLAST score 282
 E value 2.0e-25
 Match length 102
 % identity 62
 NCBI Description (AC003040) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 236884

% identity 77
 NCBI Description (AC004393) Similar to ERECTA receptor protein kinase
 gb_U47029 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 236903
 Seq. ID uC-gsronu33B008e02b1
 Method BLASTX
 NCBI GI g3603473
 BLAST score 206
 E value 4.0e-16
 Match length 76
 % identity 57

NCBI Description (AF090698) elicitor-responsive gene-3 [Oryza sativa]

Seq. No. 236904
 Seq. ID uC-gsronu33B008e04b1
 Method BLASTX
 NCBI GI g4038352
 BLAST score 239
 E value 3.0e-20
 Match length 101
 % identity 47

NCBI Description (AF098951) breast cancer resistance protein [Homo sapiens]

Seq. No. 236905
 Seq. ID uC-gsronu33B008f03b1
 Method BLASTX
 NCBI GI g2739360
 BLAST score 433
 E value 9.0e-43
 Match length 145
 % identity 63

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
 >gi_3075385 (AC004484) unknown protein [Arabidopsis
 thaliana]

Seq. No. 236906
 Seq. ID uC-gsronu33B008f10b1
 Method BLASTX
 NCBI GI g2662415
 BLAST score 173
 E value 2.0e-12
 Match length 56
 % identity 54

NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No. 236907
 Seq. ID uC-gsronu33B008f11b1
 Method BLASTX
 NCBI GI g4455190
 BLAST score 473
 E value 2.0e-47
 Match length 121
 % identity 78

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 236908

Seq. ID uC-gsronu33B008h12b1
 Method BLASTX
 NCBI GI g730463
 BLAST score 321
 E value 1.0e-29
 Match length 102
 % identity 60
 NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
 >gi_630323_pir_S44069 ribosomal protein L35a.e.c15 - yeast
 (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
 protein L37 [Saccharomyces cerevisiae]
 >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
 [Saccharomyces cerevisiae]

Seq. No. 236909
 Seq. ID uC-gsronu33B009a06b1
 Method BLASTX
 NCBI GI g2462781
 BLAST score 408
 E value 3.0e-40
 Match length 95
 % identity 75
 NCBI Description (U73175) carbamoyl phosphate synthetase small subunit
 [Arabidopsis thaliana]

Seq. No. 236910
 Seq. ID uC-gsronu33B011a09b1
 Method BLASTX
 NCBI GI g2829926
 BLAST score 186
 E value 6.0e-14
 Match length 116
 % identity 42
 NCBI Description (AC002291) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 236911
 Seq. ID uC-gsronu33B011c03b1
 Method BLASTX
 NCBI GI g1657948
 BLAST score 378
 E value 2.0e-36
 Match length 138
 % identity 89
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 236912
 Seq. ID uC-gsronu33B011d06b1
 Method BLASTX
 NCBI GI g2642432
 BLAST score 99
 E value 6.0e-09
 Match length 105
 % identity 47
 NCBI Description (AC002391) putative elicitor response element binding
 protein (WRKY3) [Arabidopsis thaliana]

Seq. No. 236913

BLAST score 193
 E value 9.0e-15
 Match length 79
 % identity 53
 NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No. 236924
 Seq. ID uC-gsronu33B012c05b1
 Method BLASTX
 NCBI GI g2213621
 BLAST score 196
 E value 5.0e-15
 Match length 50
 % identity 72
 NCBI Description (AC000103) F21J9.26 [Arabidopsis thaliana]

Seq. No. 236925
 Seq. ID uC-gsronu33B012c07b1
 Method BLASTX
 NCBI GI g3928150
 BLAST score 441
 E value 1.0e-43
 Match length 98
 % identity 90
 NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 236926
 Seq. ID uC-gsronu33B012c12b1
 Method BLASTX
 NCBI GI g3122673
 BLAST score 263
 E value 3.0e-24
 Match length 111
 % identity 57
 NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 236927
 Seq. ID uC-gsronu33B012d03b1
 Method BLASTX
 NCBI GI g984756
 BLAST score 147
 E value 3.0e-09
 Match length 90
 % identity 47
 NCBI Description (Z54153) chilling-inducible protein [Oryza sativa]

Seq. No. 236928
 Seq. ID uC-gsronu33B012e02b1
 Method BLASTX
 NCBI GI g1350707
 BLAST score 212
 E value 5.0e-17
 Match length 52
 % identity 73
 NCBI Description 60S RIBOSOMAL PROTEIN L29 >gi_539923_pir_JC2012 ribosomal protein 17K - mouse >gi_404766 (L08651) ribosomal protein

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Seq. No.          236930
Seq. ID           uC-gsronu33B012g10b1
Method            BLASTX
NCBI GI           g123379
BLAST score       141
E value           1.0e-08
Match length      31
% identity        84
NCBI Description  HMGl/2-LIKE PROTEIN (SB11 PROTEIN) >gi_99914_pir_S22309
                  HMG-1-like protein - soybean >gi_18645_emb_CAA41200-
                  (X58245) HMG-1 like protein gene [Glycine max]
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Seq. No.      236932
Seq. ID       uC-gsronu33B014e04b1
Method        BLASTX
NCBI GI       g1616614
BLAST score   207
E value       1.0e-16
Match length  40
% identity    100
NCBI Description (Y08425) small GTP-binding protein [Nicotiana
plumbaginifolia]
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>gi_83176_pir_S19389 hypothetical protein YCL059c - yeast
(Saccharomyces cerevisiae) >gi_5300_emb_CAA42386_ (X59720)
YCL059c, len:316 [Saccharomyces cerevisiae]

Seq. No. 236934
Seq. ID uC-gsronu33B014e12b1
Method BLASTX
NCBI GI g4220472
BLAST score 225
E value 4.0e-19
Match length 64
% identity 73
NCBI Description (AC006069) similar to yeast cccl protein [Arabidopsis thaliana]

Seq. No. 236935
Seq. ID uC-gsronu33B014g11b1
Method BLASTX
NCBI GI g2821957
BLAST score 141
E value 3.0e-09
Match length 56
% identity 50
NCBI Description (AB006691) spermidine synthase 2 [Hyoscyamus niger]

Seq. No. 236936
Seq. ID uC-gsronu33B015a06b1
Method BLASTX
NCBI GI g3548815
BLAST score 188
E value 4.0e-14
Match length 124
% identity 43
NCBI Description (AC005313) similar to axoneme-associated protein mst101 [Arabidopsis thaliana]

Seq. No. 236937
Seq. ID uC-gsronu33B015a07b1
Method BLASTX
NCBI GI g3924601
BLAST score 463
E value 3.0e-46
Match length 116
% identity 80
NCBI Description (AF069442) putative rac GTPase activating protein [Arabidopsis thaliana] >gi_4262138_gb_AAD14438_ (AC005275) putative rac GTPase-activating protein [Arabidopsis thaliana]

Seq. No. 236938
Seq. ID uC-gsronu33B015b06b1
Method BLASTX
NCBI GI g2465923
BLAST score 388
E value 5.0e-43
Match length 144
% identity 62

NCBI Description (AF024648) receptor-like serine/threonine kinase
[Arabidopsis thaliana]

Seq. No. 236939
Seq. ID uC-gsronu33B015b09b1
Method BLASTX
NCBI GI g4006827
BLAST score 540
E value 2.0e-55
Match length 151
% identity 77

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 236940
Seq. ID uC-gsronu33B015c07b1
Method BLASTX
NCBI GI g3668089
BLAST score 424
E value 1.0e-41
Match length 143
% identity 56

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 236941
Seq. ID uC-gsronu33B015e03b1
Method BLASTX
NCBI GI g1172441
BLAST score 384
E value 5.0e-37
Match length 160
% identity 57

NCBI Description POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi_99685_pir_S21883
DNA-binding protein POSF21 - Arabidopsis thaliana
>gi_16429_emb_CAA43366_ (X61031) posF21 [Arabidopsis
thaliana]

Seq. No. 236942
Seq. ID uC-gsronu33B015f02b1
Method BLASTX
NCBI GI g1401078
BLAST score 488
E value 3.0e-49
Match length 151
% identity 58

NCBI Description (U46691) putative chromatin structure regulator [Homo
sapiens]

Seq. No. 236943
Seq. ID uC-gsronu33B015f07b1
Method BLASTX
NCBI GI g3152596
BLAST score 372
E value 9.0e-36
Match length 131
% identity 63

NCBI Description (AC002986) YUP8H12R.36 [Arabidopsis thaliana]

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BLAST score 588
E value 5e-061
Match length 135
% identity 79
NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 236961
Seq. ID uC-gsronu33B017e10b1
Method BLASTX
NCBI GI g2281090
BLAST score 317
E value 2.0e-29
Match length 98
% identity 62
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236962
Seq. ID uC-gsronu33B017g08b1
Method BLASTX
NCBI GI g2501056
BLAST score 328
E value 4.0e-31
Match length 71
% identity 85
NCBI Description SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
>gi_2129737_pir_S71293 seryl-tRNA synthetase - Arabidopsis
thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA
Synthetase [Arabidopsis thaliana]

Seq. No. 236963
Seq. ID uC-gsronu33B018b01b1
Method BLASTX
NCBI GI g3063396
BLAST score 384
E value 8.0e-54
Match length 118
% identity 89
NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 236964
Seq. ID uC-gsronu33B018c01b1
Method BLASTX
NCBI GI g2738949
BLAST score 453
E value 3.0e-45
Match length 93
% identity 91
NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x
ananassa]

Seq. No. 236965
Seq. ID uC-gsronu33B018c12b1
Method BLASTX
NCBI GI g4510376
BLAST score 296
E value 5.0e-27
Match length 87

% identity	60
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.	236966
Seq. ID	uC-gsronu33B018d03b1
Method	BLASTX
NCBI GI	g4572674
BLAST score	274
E value	3.0e-24
Match length	61
% identity	79
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.	236967
Seq. ID	uC-gsronu33B018d07b1
Method	BLASTX
NCBI GI	g2827623
BLAST score	213
E value	4.0e-17
Match length	46
% identity	91
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]
Seq. No.	236968
Seq. ID	uC-gsronu33B018d11b1
Method	BLASTX
NCBI GI	g1657619
BLAST score	404
E value	2.0e-39
Match length	164
% identity	46
NCBI Description	(U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]
Seq. No.	236969
Seq. ID	uC-gsronu33B018f01b1
Method	BLASTX
NCBI GI	g3608412
BLAST score	334
E value	4.0e-31
Match length	99
% identity	65
NCBI Description	(AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]
Seq. No.	236970
Seq. ID	uC-gsronu33B018f10b1
Method	BLASTX
NCBI GI	g3769671
BLAST score	350
E value	4.0e-33
Match length	81
% identity	78
NCBI Description	(AF095284) Tic22 [Pisum sativum]
Seq. No.	236971
Seq. ID	uC-gsronu33B018f12b1

Method BLASTX
 NCBI GI g2738949
 BLAST score 377
 E value 2.0e-36
 Match length 84
 % identity 85
 NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No. 236972
 Seq. ID uC-gsronu33B019a03b1
 Method BLASTX
 NCBI GI g1710551
 BLAST score 281
 E value 5.0e-25
 Match length 51
 % identity 100
 NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_ (X95458) ribosomal protein L39 [Zea mays]

Seq. No. 236973
 Seq. ID uC-gsronu33B019a04b1
 Method BLASTX
 NCBI GI g3201627
 BLAST score 473
 E value 2.0e-47
 Match length 142
 % identity 64
 NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 236974
 Seq. ID uC-gsronu33B019b07b1
 Method BLASTX
 NCBI GI g2425129
 BLAST score 234
 E value 1.0e-19
 Match length 92
 % identity 53
 NCBI Description (AF020280) PkgA [Dictyostelium discoideum]

Seq. No. 236975
 Seq. ID uC-gsronu33B019c12b1
 Method BLASTX
 NCBI GI g2213592
 BLAST score 489
 E value 2.0e-49
 Match length 143
 % identity 33
 NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No. 236976
 Seq. ID uC-gsronu33B019d03b1
 Method BLASTX
 NCBI GI g2341024
 BLAST score 177
 E value 8.0e-13
 Match length 118

plumbaginifolia]

Seq. No.	236987
Seq. ID	uC-gsronu33B021c09b1
Method	BLASTX
NCBI GI	g1352681
BLAST score	419
E value	3.0e-41
Match length	128
% identity	65
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir_S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	236988
Seq. ID	uC-gsronu33B021d10b1
Method	BLASTX
NCBI GI	g4558558
BLAST score	445
E value	3.0e-44
Match length	128
% identity	66
NCBI Description	(AC007138) putative polygalacturonidase [Arabidopsis thaliana]
Seq. No.	236989
Seq. ID	uC-gsronu33B021e11b1
Method	BLASTX
NCBI GI	g2062167
BLAST score	205
E value	4.0e-16
Match length	49
% identity	76
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]
Seq. No.	236990
Seq. ID	uC-gsronu33B021e12b1
Method	BLASTX
NCBI GI	g3319353
BLAST score	255
E value	4.0e-22
Match length	73
% identity	58
NCBI Description	(AF077407) contains similarity to copper-binding proteins [Arabidopsis thaliana]
Seq. No.	236991
Seq. ID	uC-gsronu33B021f01b1
Method	BLASTX
NCBI GI	g2618686
BLAST score	189
E value	2.0e-14
Match length	89
% identity	40
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

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Seq. No.	236992
Seq. ID	uC-gsronu33B021f02b1
Method	BLASTX
NCBI GI	g3608155
BLAST score	518
E value	8.0e-53
Match length	135
% identity	68
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]
Seq. No.	236993
Seq. ID	uC-gsronu33B021h11b1
Method	BLASTX
NCBI GI	g2880046
BLAST score	260
E value	2.0e-22
Match length	110
% identity	55
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.	236994
Seq. ID	uC-gsronu33B027b01b1
Method	BLASTX
NCBI GI	g405080
BLAST score	148
E value	1.0e-09
Match length	101
% identity	40
NCBI Description	(U01058) ABC family transporter [Entamoeba histolytica]
Seq. No.	236995
Seq. ID	uC-gsronu33B027b09b1
Method	BLASTX
NCBI GI	g2245094
BLAST score	178
E value	8.0e-13
Match length	102
% identity	43
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	236996
Seq. ID	uC-gsronu33B027c11b1
Method	BLASTX
NCBI GI	g3256066
BLAST score	288
E value	2.0e-37
Match length	95
% identity	82
NCBI Description	(Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]
Seq. No.	236997
Seq. ID	uC-gsronu33B027e04b1
Method	BLASTX
NCBI GI	g2583118
BLAST score	279
E value	3.0e-25

E value 2.0e-56
 Match length 147
 % identity 74
 NCBI Description SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150)
 >gi_1173905 (U41371) spliceosome associated protein [Homo sapiens]

Seq. No. 237003
 Seq. ID uC-gsronu33B028c12b1
 Method BLASTX
 NCBI GI g282881
 BLAST score 510
 E value 7.0e-52
 Match length 138
 % identity 67
 NCBI Description receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 237004
 Seq. ID uC-gsronu33B028h03b1
 Method BLASTX
 NCBI GI g2342682
 BLAST score 208
 E value 5.0e-17
 Match length 50
 % identity 74
 NCBI Description (AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No. 237005
 Seq. ID uC-gsronu33B029b10b1
 Method BLASTX
 NCBI GI g3860250
 BLAST score 233
 E value 8.0e-20
 Match length 50
 % identity 90
 NCBI Description (AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No. 237006
 Seq. ID uC-gsronu33B029b11b1
 Method BLASTX
 NCBI GI g4324597
 BLAST score 102
 E value 6.0e-09
 Match length 95
 % identity 45
 NCBI Description (AF106324) sodium proton exchanger Nhx1 [Arabidopsis thaliana]

Seq. No. 237007
 Seq. ID uC-gsronu33B029d09b1
 Method BLASTX
 NCBI GI g171366
 BLAST score 253

E value 1.0e-21
 Match length 158
 % identity 35
 NCBI Description (M69294) alantoinase [*Saccharomyces cerevisiae*]

Seq. No. 237008
 Seq. ID uC-gsronu33B029f12b1
 Method BLASTX
 NCBI GI g1184123
 BLAST score 228
 E value 9.0e-19
 Match length 79
 % identity 54
 NCBI Description (U20809) auxin-induced protein [*Vigna radiata*]

Seq. No. 237009
 Seq. ID uC-gsronu33B031a07b1
 Method BLASTX
 NCBI GI g3033377
 BLAST score 410
 E value 4.0e-40
 Match length 137
 % identity 55
 NCBI Description (AC004238) putative berberine bridge enzyme [*Arabidopsis thaliana*]

Seq. No. 237010
 Seq. ID uC-gsronu33B031b03b1
 Method BLASTX
 NCBI GI g4103635
 BLAST score 328
 E value 2.0e-30
 Match length 94
 % identity 64
 NCBI Description (AF026538) ABA-responsive protein [*Hordeum vulgare*]

Seq. No. 237011
 Seq. ID uC-gsronu33B031b10b1
 Method BLASTX
 NCBI GI g3549660
 BLAST score 341
 E value 5.0e-32
 Match length 123
 % identity 56
 NCBI Description (AL031394) carbonate dehydratase - like protein [*Arabidopsis thaliana*]

Seq. No. 237012
 Seq. ID uC-gsronu33B031e03b1
 Method BLASTX
 NCBI GI g2738949
 BLAST score 290
 E value 3.0e-26
 Match length 90
 % identity 66
 NCBI Description (AF022213) cytosolic ascorbate peroxidase [*Fragaria x ananassa*]

Seq. No. 237013
 Seq. ID uC-gsronu33B031g01b1
 Method BLASTX
 NCBI GI g2384760
 BLAST score 189
 E value 2.0e-14
 Match length 47
 % identity 74
 NCBI Description (AF016897) GDP dissociation inhibitor protein OsgDI2 [Oryza sativa]

Seq. No. 237014
 Seq. ID uC-gsronu33B031g08b1
 Method BLASTX
 NCBI GI g3548802
 BLAST score 185
 E value 3.0e-14
 Match length 53
 % identity 64
 NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]
 >gi_4335769_gb_AAD17446_ (AC006284) putative axil protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 237015
 Seq. ID uC-gsronu33B031h06b1
 Method BLASTX
 NCBI GI g3402704
 BLAST score 469
 E value 6.0e-47
 Match length 138
 % identity 74
 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237016
 Seq. ID uC-gsronu33B032c03b1
 Method BLASTX
 NCBI GI g3461846
 BLAST score 300
 E value 1.0e-27
 Match length 84
 % identity 36
 NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No. 237017
 Seq. ID uC-gsronu33B032g02b1
 Method BLASTX
 NCBI GI g2129742
 BLAST score 275
 E value 3.0e-24
 Match length 77
 % identity 65
 NCBI Description stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related

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Method BLASTX
 NCBI GI g2253583
 BLAST score 294
 E value 1.0e-26
 Match length 96
 % identity 66
 NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237024
 Seq. ID uC-gsronu33B036f08b1
 Method BLASTX
 NCBI GI g2443887
 BLAST score 614
 E value 5.0e-64
 Match length 152
 % identity 76
 NCBI Description (AC002294) Similar to transcription factor gb_246606_1658307 and others [Arabidopsis thaliana]

Seq. No. 237025
 Seq. ID uC-gsronu33B036h01b1
 Method BLASTX
 NCBI GI g1170409
 BLAST score 188
 E value 4.0e-14
 Match length 61
 % identity 67
 NCBI Description HOMEBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22) >gi_549887 (U09336) homeobox protein [Arabidopsis thaliana] >gi_549888 (U09337) homeobox protein [Arabidopsis thaliana] >gi_4490724_emb_CAB38927.1_ (AL035709) homeobox protein HAT22 [Arabidopsis thaliana]

Seq. No. 237026
 Seq. ID uC-gsronu33B037b05b1
 Method BLASTX
 NCBI GI g881625
 BLAST score 319
 E value 2.0e-29
 Match length 70
 % identity 80
 NCBI Description (U29432) 22.8 kDa protein [Ipomoea trifida]

Seq. No. 237027
 Seq. ID uC-gsronu33B037b06b1
 Method BLASTX
 NCBI GI g1076685
 BLAST score 358
 E value 3.0e-34
 Match length 103
 % identity 44
 NCBI Description SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_ (D30038) SPF1 protein [Ipomoea batatas]

Seq. No. 237028
 Seq. ID uC-gsronu33B037b10b1
 Method BLASTX

NCBI GI g3738089
 BLAST score 231
 E value 2.0e-19
 Match length 86
 % identity 59
 NCBI Description (AC005617) similar to symbiotic ammonium transporter, SAT1 [Arabidopsis thaliana] >gi_4314372_gb_AAD15583_ (AC006340) putative symbiotic ammonium transporter SAT1 [Arabidopsis thaliana]

Seq. No. 237029
 Seq. ID uC-gsronu33B037c09b1
 Method BLASTX
 NCBI GI g4263722
 BLAST score 312
 E value 5.0e-29
 Match length 90
 % identity 67
 NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 237030
 Seq. ID uC-gsronu33B037f01b1
 Method BLASTX
 NCBI GI g3033380
 BLAST score 430
 E value 1.0e-42
 Match length 102
 % identity 80
 NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No. 237031
 Seq. ID uC-gsronu33B037f05b1
 Method BLASTX
 NCBI GI g3953471
 BLAST score 222
 E value 3.0e-18
 Match length 53
 % identity 70
 NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 237032
 Seq. ID uC-gsronu33B037f12b1
 Method BLASTX
 NCBI GI g3548802
 BLAST score 372
 E value 1.0e-35
 Match length 141
 % identity 51
 NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axil protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 237033
 Seq. ID uC-gsronu33B037g07b1
 Method BLASTX
 NCBI GI g3986110

NCBI Description (AF003197) glutamine synthetase [Hevea brasiliensis]

Seq. No. 237039
Seq. ID uC-gsronu33B038e03b1
Method BLASTX
NCBI GI g1938424
BLAST score 267
E value 2.0e-23
Match length 148
% identity 39

NCBI Description (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]

Seq. No. 237040
Seq. ID uC-gsronu33B038e09b1
Method BLASTX
NCBI GI g3600033
BLAST score 475
E value 1.0e-47
Match length 168
% identity 54

NCBI Description (AF080119) contains similarity to the N terminal domain of the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis thaliana]

Seq. No. 237041
Seq. ID uC-gsronu33B038e11b1
Method BLASTX
NCBI GI g2244868
BLAST score 562
E value 6.0e-58
Match length 115
% identity 89
NCBI Description (Z97337) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 237042
Seq. ID uC-gsronu33B038f12b1
Method BLASTX
NCBI GI g4566614
BLAST score 186
E value 3.0e-14
Match length 47
% identity 77
NCBI Description (AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No. 237043
Seq. ID uC-gsronu33B038g07b1
Method BLASTX
NCBI GI g3096922
BLAST score 293
E value 2.0e-26
Match length 84
% identity 69
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 237044

Seq. ID uC-gsronu33B038h03b1
 Method BLASTX
 NCBI GI g2262113
 BLAST score 238
 E value 6.0e-20
 Match length 74
 % identity 72
 NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 237045
 Seq. ID uC-gsronu33B038h10b1
 Method BLASTX
 NCBI GI g1297187
 BLAST score 568
 E value 1.0e-58
 Match length 162
 % identity 69
 NCBI Description (U53501) similar to protein encoded by GenBank Accession Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No. 237046
 Seq. ID uC-gsronu33B039f07b1
 Method BLASTX
 NCBI GI g3860256
 BLAST score 358
 E value 2.0e-34
 Match length 91
 % identity 71
 NCBI Description (AC005824) putative tRNA isopentenylpyrophosphate transferase [Arabidopsis thaliana]

Seq. No. 237047
 Seq. ID uC-gsronu33B039h03b1
 Method BLASTX
 NCBI GI g4335729
 BLAST score 201
 E value 8.0e-16
 Match length 108
 % identity 5
 NCBI Description (AC006248) putative salt-inducible protein [Arabidopsis thaliana]

Seq. No. 237048
 Seq. ID uC-gsronu33B040a09b1
 Method BLASTX
 NCBI GI g2459435
 BLAST score 144
 E value 2.0e-09
 Match length 42
 % identity 62
 NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 237049
 Seq. ID uC-gsronu33B040b01b1
 Method BLASTX
 NCBI GI g3395436

% identity 61
NCBI Description (297344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237055
Seq. ID uC-gsronu33B041h07b1
Method BLASTX
NCBI GI g3850823
BLAST score 190
E value 7.0e-15
Match length 70

% identity 56
NCBI Description (Y18351) U2 snRNP auxiliary factor, large subunit
[Nicotiana glauca]

Seq. No. 237056
Seq. ID uC-gsronu33B041h09b1
Method BLASTX
NCBI GI g1173218

BLAST score 326
E value 2.0e-30
Match length 62

% identity 100
NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No. 237057
Seq. ID uC-gsronu33B042d02b1
Method BLASTX
NCBI GI g3510505

BLAST score 307
E value 4.0e-28
Match length 130

% identity 44
NCBI Description (AF030881) pol polyprotein [Fugu rubripes]

Seq. No. 237058
Seq. ID uC-gsronu33B042e04b1
Method BLASTX

NCBI GI g3924603
BLAST score 307
E value 1.0e-28
Match length 76

% identity 53
NCBI Description (AF069442) putative WD-repeat protein [Arabidopsis
thaliana]

Seq. No. 237059
Seq. ID uC-gsronu33B042f03b1
Method BLASTX

NCBI GI g417540
BLAST score 388
E value 2.0e-37
Match length 117

% identity 67
NCBI Description PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
>gi_20851_emb_CAA44646_ (X62842) pyrroline carboxylate

reductase [Pisum sativum] >gi_445614_prf_1909360A
pyrroline carboxylate reductase [Pisum sativum]

Seq. No. 237060
Seq. ID uC-gsronu33B042f08b1
Method BLASTX
NCBI GI g4539298
BLAST score 498
E value 2.0e-50
Match length 148
% identity 64
NCBI Description (AL049480) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No. 237061
Seq. ID uC-gsronu33B042f09b1
Method BLASTX
NCBI GI g294668
BLAST score 198
E value 7.0e-16
Match length 41
% identity 98
NCBI Description (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No. 237062
Seq. ID uC-gsronu33B044a02b1
Method BLASTX
NCBI GI g4127461
BLAST score 241
E value 6.0e-21
Match length 58
% identity 81
NCBI Description (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]

Seq. No. 237063
Seq. ID uC-gsronu33B044a09b1
Method BLASTX
NCBI GI g3193301
BLAST score 183
E value 3.0e-14
Match length 73
% identity 47
NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No. 237064
Seq. ID uC-gsronu33B044d03b1
Method BLASTX
NCBI GI g2995405
BLAST score 190
E value 6.0e-15
Match length 51
% identity 76
NCBI Description (Y12432) polyprotein [Ananas comosus]

Seq. No. 237065
 Seq. ID uC-gsronu33B044e12b1
 Method BLASTX
 NCBI GI g1173209
 BLAST score 600
 E value 2.0e-62
 Match length 120
 % identity 99
 NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal protein S16 protein - upland cotton
 >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No. 237066
 Seq. ID uC-gsronu33B044g05b1
 Method BLASTX
 NCBI GI g2335101
 BLAST score 523
 E value 2.0e-53
 Match length 117
 % identity 79
 NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 237067
 Seq. ID uC-gsronu33B046a03b1
 Method BLASTX
 NCBI GI g2465923
 BLAST score 474
 E value 1.0e-47
 Match length 122
 % identity 73
 NCBI Description (AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 237068
 Seq. ID uC-gsronu33B046c04b1
 Method BLASTX
 NCBI GI g1076275
 BLAST score 202
 E value 2.0e-16
 Match length 43
 % identity 93
 NCBI Description phenylalanine ammonia-lyase - muskmelon
 >gi_735957_emb_CAA53733_ (X76130) phenylalanine ammonia-lyase [Cucumis melo]

Seq. No. 237069
 Seq. ID uC-gsronu33B046c07b1
 Method BLASTX
 NCBI GI g2739279
 BLAST score 170
 E value 4.0e-12
 Match length 77
 % identity 43
 NCBI Description (AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

E value 2.0e-27
 Match length 102
 % identity 59
 NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 237076
 Seq. ID uC-gsronu33B047b02b1
 Method BLASTX
 NCBI GI g2493852
 BLAST score 291
 E value 4.0e-26
 Match length 63
 % identity 84
 NCBI Description CYTOCHROME C OXIDASE POLYPEPTIDE VC
 >gi_1070356_emb_CAA92107_ (Z68091) cytochrome c oxidase, Vc subunit [Hordeum vulgare]

Seq. No. 237077
 Seq. ID uC-gsronu33B047b08b1
 Method BLASTX
 NCBI GI g2760327
 BLAST score 498
 E value 1.0e-50
 Match length 109
 % identity 44
 NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No. 237078
 Seq. ID uC-gsronu33B047e03b1
 Method BLASTX
 NCBI GI g1076793
 BLAST score 638
 E value 7.0e-67
 Match length 138
 % identity 62
 NCBI Description calmodulin, cam2 - maize >gi_747917_emb_CAA54583_ (X77397)
 calmodulin [Zea mays]

Seq. No. 237079
 Seq. ID uC-gsronu33B047f02b1
 Method BLASTX
 NCBI GI g2626753
 BLAST score 522
 E value 4.0e-53
 Match length 168
 % identity 65
 NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No. 237080
 Seq. ID uC-gsronu33B048b01b1
 Method BLASTX
 NCBI GI g4538911
 BLAST score 180
 E value 3.0e-13
 Match length 119
 % identity 32

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237081
Seq. ID uC-gsronu33B048e02b1
Method BLASTX
NCBI GI g2244749
BLAST score 499
E value 8.0e-51
Match length 98
% identity 94

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 237082
Seq. ID uC-gsronu33B048e05b1
Method BLASTX
NCBI GI g2098705
BLAST score 534
E value 1.0e-56
Match length 153
% identity 77

NCBI Description (U82973) pectinesterase [Citrus sinensis]

Seq. No. 237083
Seq. ID uC-gsronu33B048e08b1
Method BLASTX
NCBI GI g2244949
BLAST score 265
E value 2.0e-23
Match length 72
% identity 75
NCBI Description (Z97339) similarity to ORF - Lilium longiflorum [Arabidopsis thaliana]

Seq. No. 237084
Seq. ID uC-gsronu33B048e12b1
Method BLASTX
NCBI GI g2078350
BLAST score 212
E value 5.0e-17
Match length 108
% identity 44
NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 237085
Seq. ID uC-gsronu33B048g02b1
Method BLASTX
NCBI GI g3687389
BLAST score 339
E value 3.0e-32
Match length 78
% identity 85
NCBI Description (Y16124) putative cullin protein [Lycopersicon esculentum]

Seq. No. 237086
Seq. ID uC-gsronu33B049a03b1
Method BLASTX
NCBI GI g4469025

Seq. No. 237103
 Seq. ID uC-gsronu33B055d07b1
 Method BLASTX
 NCBI GI g4049401
 BLAST score 185
 E value 5.0e-14
 Match length 51
 % identity 67
 NCBI Description (AJ131580) glutathione transferase AtGST 10 [Arabidopsis thaliana]

Seq. No. 237104
 Seq. ID uC-gsronu33B055d09b1
 Method BLASTX
 NCBI GI g1169200
 BLAST score 313
 E value 2.0e-29
 Match length 73
 % identity 79
 NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR >gi_421829_pir_S33706 DNA-damage resistance protein - Arabidopsis thaliana >gi_166694 (M98455) [Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT111) mRNA, complete cds.], gene product [Arabidopsis thaliana]

Seq. No. 237105
 Seq. ID uC-gsronu33B055e08b1
 Method BLASTX
 NCBI GI g1019946
 BLAST score 149
 E value 4.0e-10
 Match length 33
 % identity 82
 NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]

Seq. No. 237106
 Seq. ID uC-gsronu33B055f08b1
 Method BLASTX
 NCBI GI g730456
 BLAST score 309
 E value 1.0e-28
 Match length 68
 % identity 81
 NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 237107
 Seq. ID uC-gsronu33B055h04b1
 Method BLASTX
 NCBI GI g4468805
 BLAST score 256
 E value 2.0e-22
 Match length 84
 % identity 56
 NCBI Description (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No. 237108
 Seq. ID uC-gsronu33B057a11b1
 Method BLASTX
 NCBI GI g2224897
 BLAST score 275
 E value 2.0e-24
 Match length 118
 % identity 53
 NCBI Description (U67132) DNA-binding protein PcMYB1 [Petroselinum crispum]

Seq. No. 237109
 Seq. ID uC-gsronu33B057b08b1
 Method BLASTX
 NCBI GI g2984292
 BLAST score 184
 E value 2.0e-17
 Match length 108
 % identity 48
 NCBI Description (AE000771) GTP-binding protein [Aquifex aeolicus]

Seq. No. 237110
 Seq. ID uC-gsronu33B057d12b1
 Method BLASTX
 NCBI GI g4539348
 BLAST score 136
 E value 1.0e-17
 Match length 95
 % identity 52
 NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No. 237111
 Seq. ID uC-gsronu33B057f05b1
 Method BLASTX
 NCBI GI g4510345
 BLAST score 222
 E value 1.0e-18
 Match length 48
 % identity 81
 NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 237112
 Seq. ID uC-gsronu33B057g04b1
 Method BLASTX
 NCBI GI g1352186
 BLAST score 325
 E value 2.0e-30
 Match length 89
 % identity 70
 NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No. 237113
 Seq. ID uC-gsronu33B057g08b1
 Method BLASTX
 NCBI GI g529353

BLAST score 219
 E value 9.0e-18
 Match length 125
 % identity 51
 NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 237114
 Seq. ID uC-gsronu33B057h03b1
 Method BLASTX
 NCBI GI g2665890
 BLAST score 358
 E value 4.0e-34
 Match length 86
 % identity 78
 NCBI Description (AF035944) calcium-dependent protein kinase [Fragaria x ananassa]

Seq. No. 237115
 Seq. ID uC-gsronu33B057h10b1
 Method BLASTX
 NCBI GI g2194115
 BLAST score 197
 E value 1.0e-15
 Match length 70
 % identity 56
 NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No. 237116
 Seq. ID uC-gsronu33B058a07b1
 Method BLASTX
 NCBI GI g2827141
 BLAST score 158
 E value 1.0e-10
 Match length 36
 % identity 78
 NCBI Description (AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 237117
 Seq. ID uC-gsronu33B058a09b1
 Method BLASTX
 NCBI GI g2465008
 BLAST score 459
 E value 6.0e-46
 Match length 140
 % identity 63
 NCBI Description (AJ001445) ripening-induced protein [Fragaria vesca]

Seq. No. 237118
 Seq. ID uC-gsronu33B058a10b1
 Method BLASTX
 NCBI GI g3122386
 BLAST score 656
 E value 5.0e-69
 Match length 130
 % identity 47
 NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi_2394227 (AF016845) WD-40

repeat protein [Lycopersicon esculentum]

Seq. No. 237119
 Seq. ID uC-gsronu33B058c08b1
 Method BLASTX
 NCBI GI g2137156
 BLAST score 142
 E value 7.0e-09
 Match length 92
 % identity 45
 NCBI Description apoptosis protein MA-3 - mouse >gi_1384078_dbj_BAA09056_ (D50465) apoptosis-inducible [Mus musculus]

Seq. No. 237120
 Seq. ID uC-gsronu33B058c10b1
 Method BLASTX
 NCBI GI g3582333
 BLAST score 236
 E value 9.0e-20
 Match length 133
 % identity 37
 NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237121
 Seq. ID uC-gsronu33B058e03b1
 Method BLASTX
 NCBI GI g4455356
 BLAST score 550
 E value 1.0e-56
 Match length 144
 % identity 74
 NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 237122
 Seq. ID uC-gsronu33B058f12b1
 Method BLASTX
 NCBI GI g4314396
 BLAST score 153
 E value 4.0e-10
 Match length 54
 % identity 57
 NCBI Description (AC006232) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No. 237123
 Seq. ID uC-gsronu33B058g09b1
 Method BLASTX
 NCBI GI g4006878
 BLAST score 484
 E value 7.0e-49
 Match length 124
 % identity 72
 NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No. 237124
 Seq. ID uC-gsronu33B058h03b1
 Method BLASTX

NCBI Description PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE
(RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)

Seq. No. 237145
Seq. ID uC-gsronu33B076c03b1
Method BLASTX
NCBI GI g1469930
BLAST score 181
E value 1.0e-13
Match length 45
% identity 82
NCBI Description (U48777) fiber-specific acyl carrier protein [Gossypium
hirsutum]

Seq. No. 237146
Seq. ID uC-gsronu33B076c12b1
Method BLASTX
NCBI GI g548770
BLAST score 159
E value 4.0e-11
Match length 36
% identity 83
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal
protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
ribosomal protein L3 [Oryza sativa]

Seq. No. 237147
Seq. ID uC-gsronu33B076f02b1
Method BLASTX
NCBI GI g3098571
BLAST score 232
E value 2.0e-19
Match length 82
% identity 51
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]

Seq. No. 237148
Seq. ID uC-gsronu33B076g03b1
Method BLASTX
NCBI GI g3193234
BLAST score 156
E value 2.0e-10
Match length 43
% identity 67
NCBI Description (AF068690) peroxisomal targeting signal-1 receptor
[Citrullus lanatus]

Seq. No. 237149
Seq. ID uC-gsronu33B077a08b1
Method BLASTX
NCBI GI g2058280
BLAST score 198
E value 7.0e-16
Match length 37
% identity 97
NCBI Description (X97381) atran3 [Arabidopsis thaliana]

Match length 72
 % identity 81
 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
 (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
 3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir_S40146
 catechol O-methyltransferase (EC 2.1.1.6) - cider tree
 >gi_437777_emb_CAA52814_ (X74814) O-Methyltransferase
 [Eucalyptus gunnii]

Seq. No. 237177
 Seq. ID uC-gsronu33B079c09b1
 Method BLASTX
 NCBI GI g136644
 BLAST score 247
 E value 5.0e-21
 Match length 59
 % identity 80
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_100765_pir_A34506
 23K ubiquitin carrier protein E2 - wheat >gi_170782
 (M28059) ubiquitin carrier protein [Triticum vulgare]

Seq. No. 237178
 Seq. ID uC-gsronu33B079c11b1
 Method BLASTX
 NCBI GI g3319353
 BLAST score 225
 E value 1.0e-18
 Match length 74
 % identity 64
 NCBI Description (AF077407) contains similarity to copper-binding proteins
 [Arabidopsis thaliana]

Seq. No. 237179
 Seq. ID uC-gsronu33B079e03b1
 Method BLASTX
 NCBI GI g3668118
 BLAST score 378
 E value 1.0e-36
 Match length 93
 % identity 75
 NCBI Description (AJ224078) hypothetical protein [Brassica napus]

Seq. No. 237180
 Seq. ID uC-gsronu33B079e10b1
 Method BLASTX
 NCBI GI g1076627
 BLAST score 414
 E value 8.0e-41
 Match length 91
 % identity 88
 NCBI Description inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco
 >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase
 [Nicotiana tabacum]

Seq. No. 237181
 Seq. ID uC-gsronu33B079e11b1

Seq. No. 237191
 Seq. ID uC-gsronu33B080e11b1
 Method BLASTX
 NCBI GI g3158474
 BLAST score 635
 E value 2.0e-66
 Match length 137
 % identity 89
 NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 237192
 Seq. ID uC-gsronu33B080e12b1
 Method BLASTX
 NCBI GI g3355468
 BLAST score 522
 E value 3.0e-53
 Match length 120
 % identity 89
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 237193
 Seq. ID uC-gsronu33B080f12b1
 Method BLASTX
 NCBI GI g4559346
 BLAST score 242
 E value 2.0e-20
 Match length 91
 % identity 45
 NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No. 237194
 Seq. ID uC-gsronu33B080g03b1
 Method BLASTX
 NCBI GI g1563719
 BLAST score 324
 E value 4.0e-30
 Match length 68
 % identity 88
 NCBI Description (Y08320) cyclophylin [Digitalis lanata]

Seq. No. 237195
 Seq. ID uC-gsronu33B080h03b1
 Method BLASTX
 NCBI GI g4572679
 BLAST score 280
 E value 3.0e-25
 Match length 71
 % identity 77
 NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No. 237196
 Seq. ID uC-gsronu33B080h08b1
 Method BLASTX
 NCBI GI g3850816
 BLAST score 235

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 237212
Seq. ID uC-gsronu33B086d12b1
Method BLASTX
NCBI GI g4185819
BLAST score 192
E value 5.0e-15
Match length 47
% identity 68

NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No. 237213
Seq. ID uC-gsronu33B086e02b1
Method BLASTX
NCBI GI g2959781
BLAST score 180
E value 9.0e-14
Match length 39
% identity 87

NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 237214
Seq. ID uC-gsronu33B086g12b1
Method BLASTX
NCBI GI g2244898
BLAST score 220
E value 2.0e-18
Match length 45
% identity 96
NCBI Description (Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 237215
Seq. ID uC-gsronu33B086h10b1
Method BLASTX
NCBI GI g99749
BLAST score 204
E value 1.0e-16
Match length 38
% identity 95
NCBI Description probable serine/threonine-specific protein kinase ATPK64 (EC 2.7.1.-) - Arabidopsis thaliana
>gi_217843_dbj_BAA01731_ (D10937) protein kinase [Arabidopsis thaliana]

Seq. No. 237216
Seq. ID uC-gsronu33B087c05b1
Method BLASTX
NCBI GI g4008072
BLAST score 164
E value 1.0e-11
Match length 66
% identity 45
NCBI Description (AF105425) chitinase [Cynodon dactylon]

Seq. No. 237217
 Seq. ID uC-gsronu33B087f01b1
 Method BLASTX
 NCBI GI g1168408
 BLAST score 161
 E value 2.0e-11
 Match length 38
 % identity 82
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
 >gi_2118268_pir_S58168 fructose-bisphosphate aldolase (EC
 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)
 fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 237218
 Seq. ID uC-gsronu33B087f08b1
 Method BLASTX
 NCBI GI g3420008
 BLAST score 238
 E value 5.0e-20
 Match length 106
 % identity 42
 NCBI Description (AF000307) steroid sulfotransferase 3 [Brassica napus]

Seq. No. 237219
 Seq. ID uC-gsronu33B087h07b1
 Method BLASTX
 NCBI GI g3482929
 BLAST score 147
 E value 9.0e-10
 Match length 28
 % identity 93
 NCBI Description (AC003970) Putative transcription factor [Arabidopsis
 thaliana]

Seq. No. 237220
 Seq. ID uC-gsronu33B089b08b1
 Method BLASTX
 NCBI GI g2462828
 BLAST score 247
 E value 2.0e-21
 Match length 87
 % identity 53
 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237221
 Seq. ID uC-gsronu33B089b11b1
 Method BLASTX
 NCBI GI g4115377
 BLAST score 169
 E value 6.0e-12
 Match length 53
 % identity 75
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 237222
 Seq. ID uC-gsronu33B089c05b1
 Method BLASTX

09634016 101000

NCBI GI g416650
BLAST score 400
E value 6.0e-39
Match length 112
% identity 68
NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT35/PCNT111) >gi_100304_pir_S16268 auxin-induced protein (clone pGNT35) - common tobacco
>gi_19797_emb_CAA39706_ (X56265) auxin-induced protein [Nicotiana tabacum] >gi_19801_emb_CAA39710_ (X56269) auxin-induced protein [Nicotiana tabacum]

Seq. No. 237223
Seq. ID uC-gsronu33B089d08b1
Method BLASTX
NCBI GI g3395440
BLAST score 339
E value 1.0e-44
Match length 135
% identity 64
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237224
Seq. ID uC-gsronu33B089e01b1
Method BLASTX
NCBI GI g1168470
BLAST score 570
E value 6.0e-59
Match length 121
% identity 89
NCBI Description PROTEIN KINASE APK1A >gi_282877_pir_S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No. 237225
Seq. ID uC-gsronu33B089f09b1
Method BLASTX
NCBI GI g1946329
BLAST score 446
E value 2.0e-44
Match length 123
% identity 68
NCBI Description (U69154) prohibitin [Nicotiana tabacum]

Seq. No. 237226
Seq. ID uC-gsronu33B089h12b1
Method BLASTX
NCBI GI g125606
BLAST score 141
E value 8.0e-09
Match length 55
% identity 56
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248 pyruvate kinase (EC 2.7.1.40) - potato
>gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum

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Seq. No.      237228
Seq. ID       uC-gsronu33B090e06b1
Method        BLASTX
NCBI GI       g2909781
BLAST score   261
E value       1.0e-22
Match length  120
% identity    47
NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump
                [Arabidopsis thaliana]
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Seq. No.	237230
Seq. ID	uC-gsronu33B090f06b1
Method	BLASTX
NCBI GI	g4056456
BLAST score	177
E value	8.0e-13
Match length	101
% identity	46
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

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Seq. No.	237232
Seq. ID	uC-gsronu33B096g02b1
Method	BLASTX
NCBI GI	g3860250
BLAST score	543
E value	7.0e-56
Match length	118
% identity	89
NCBI Description	(AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]
Seq. No.	237233
Seq. ID	uC-gsronu33B098a02b1
Method	BLASTX
NCBI GI	g1168727
BLAST score	167
E value	5.0e-12
Match length	42
% identity	86
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_474300_dbj_BAA03099_ (D13991) cinnamyl alcohol dehydrogenase [Aralia cordata] >gi_745086_prf_2015401A cinnamoyl alcohol dehydrogenase [Aralia cordata]
Seq. No.	237234
Seq. ID	uC-gsronu33B098a04b1
Method	BLASTX
NCBI GI	g1076609
BLAST score	243
E value	8.0e-21
Match length	50
% identity	86
NCBI Description	NTL1 protein - curled-leaved tobacco
Seq. No.	237235
Seq. ID	uC-gsronu33B098a11b1
Method	BLASTX
NCBI GI	g4455159
BLAST score	283
E value	3.0e-32
Match length	86
% identity	79
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]
Seq. No.	237236
Seq. ID	uC-gsronu33B098e05b1
Method	BLASTX
NCBI GI	g4158219
BLAST score	484
E value	8.0e-49
Match length	138
% identity	67
NCBI Description	(Y18623) amylogenin [Oryza sativa]
Seq. No.	237237
Seq. ID	uC-gsronu33B098h04b1
Method	BLASTX

NCBI GI g2765748
 BLAST score 180
 E value 3.0e-13
 Match length 41
 % identity 85
 NCBI Description (Z93764) PaMip-2 [Picea abies]

Seq. No. 237238
 Seq. ID uC-gsronu33B099a06b1
 Method BLASTX
 NCBI GI g1915974
 BLAST score 160
 E value 3.0e-11
 Match length 45
 % identity 71
 NCBI Description (U62329) fructokinase [Lycopersicon esculentum] >gi_2102693
 (U64818) fructokinase [Lycopersicon esculentum]

Seq. No. 237239
 Seq. ID uC-gsronu33B099a07b1
 Method BLASTX
 NCBI GI g3193310
 BLAST score 303
 E value 1.0e-27
 Match length 113
 % identity 55
 NCBI Description (AF069300) contains similarity to Nicotiana tabacum hin1
 (GB:Y07563) [Arabidopsis thaliana]

Seq. No. 237240
 Seq. ID uC-gsronu33B099b08b1
 Method BLASTX
 NCBI GI g1084455
 BLAST score 170
 E value 2.0e-12
 Match length 38
 % identity 89
 NCBI Description peptidylprolyl isomerase (EC 5.2.1.8). Cyp2 - rice
 >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 237241
 Seq. ID uC-gsronu33B099c03b1
 Method BLASTX
 NCBI GI g3142300
 BLAST score 389
 E value 1.0e-37
 Match length 118
 % identity 64
 NCBI Description (AC002411) Contains similarity to pre-mRNA processing
 protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908
 and gb_T88158, gb_N38703 and gb_AA651043 come from this
 gene. [Arabidopsis thaliana]

Seq. No. 237242
 Seq. ID uC-gsronu33B099c09b1
 Method BLASTX
 NCBI GI g2811025

BLAST score 612
 E value 7.0e-64
 Match length 136
 % identity 82
 NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
 (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 237243
 Seq. ID uC-gsronu33B099d02b1
 Method BLASTX
 NCBI GI g4200165
 BLAST score 721
 E value 1.0e-76
 Match length 145
 % identity 86
 NCBI Description (Y16262) neutral invertase [Daucus carota]

Seq. No. 237244
 Seq. ID uC-gsronu33B099d05b1
 Method BLASTX
 NCBI GI g3540207
 BLAST score 344
 E value 2.0e-32
 Match length 102
 % identity 71
 NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 237245
 Seq. ID uC-gsronu33B099d10b1
 Method BLASTX
 NCBI GI g642339
 BLAST score 199
 E value 2.0e-15
 Match length 99
 % identity 47
 NCBI Description (X83226) peroxisome biogenesis invlved proteind
 [Saccharomyces cerevisiae]

Seq. No. 237246
 Seq. ID uC-gsronu33B099e07b1
 Method BLASTX
 NCBI GI g1172571
 BLAST score 517
 E value 9.0e-53
 Match length 126
 % identity 97
 NCBI Description PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)
 >gi_1076277_pir_S52637 phosphoenolpyruvate carboxykinase
 (ATP) (EC 4.1.1.49) - cucumber >gi_567102 (L31899)
 phosphoenolpyruvate carboxykinase [Cucumis sativus]

Seq. No. 237247
 Seq. ID uC-gsronu33B099e11b1
 Method BLASTX
 NCBI GI g2632105
 BLAST score 586
 E value 9.0e-61

NCBI GI g2880049
 BLAST score 208
 E value 2.0e-16
 Match length 44
 % identity 91
 NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237253
 Seq. ID uC-gsronu33B099h06b1
 Method BLASTX
 NCBI GI g4539423
 BLAST score 270
 E value 9.0e-24
 Match length 77
 % identity 71
 NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No. 237254
 Seq. ID uC-gsronu33B099h09b1
 Method BLASTX
 NCBI GI g2707336
 BLAST score 291
 E value 4.0e-26
 Match length 81
 % identity 69
 NCBI Description (AF037442) histone acetyltransferase [Arabidopsis thaliana]

Seq. No. 237255
 Seq. ID uC-gsronu33B100c05b1
 Method BLASTX
 NCBI GI g2443329
 BLAST score 149
 E value 4.0e-10
 Match length 36
 % identity 83
 NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 237256
 Seq. ID uC-gsronu33B100d11b1
 Method BLASTX
 NCBI GI g4263517
 BLAST score 142
 E value 3.0e-09
 Match length 78
 % identity 46
 NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana]

Seq. No. 237257
 Seq. ID uC-gsronu33B100g02b1
 Method BLASTX
 NCBI GI g4521249
 BLAST score 417
 E value 4.0e-41

Match length 121
 % identity 68
 NCBI Description (AB013912) DNA helicase [Mus musculus]

Seq. No. 237258
 Seq. ID uC-gsronu33B100g05b1
 Method BLASTX
 NCBI GI g2462751
 BLAST score 168
 E value 4.0e-12
 Match length 36
 % identity 92
 NCBI Description (AC002292) nearly identical to rice water stress induced protein gp_D26537_537404 [Arabidopsis thaliana]

Seq. No. 237259
 Seq. ID uC-gsronu33B100g12b1
 Method BLASTX
 NCBI GI g2911799
 BLAST score 214
 E value 9.0e-18
 Match length 48
 % identity 90
 NCBI Description (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No. 237260
 Seq. ID uC-gsronu33B101a03b1
 Method BLASTX
 NCBI GI g4038035
 BLAST score 231
 E value 9.0e-20
 Match length 60
 % identity 82
 NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No. 237261
 Seq. ID uC-gsronu33B101f02b1
 Method BLASTX
 NCBI GI g4567312
 BLAST score 464
 E value 1.0e-46
 Match length 113
 % identity 75
 NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237262
 Seq. ID uC-gsronu33B103a02b1
 Method BLASTX
 NCBI GI g3164115
 BLAST score 228
 E value 7.0e-19
 Match length 114
 % identity 40
 NCBI Description (AJ224145) major latex-like protein [Rubus idaeus]

Seq. No.	237263
Seq. ID	uC-gsronu33B103b01b1
Method	BLASTX
NCBI GI	g2244876
BLAST score	363
E value	1.0e-34
Match length	93
% identity	70
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237264
Seq. ID	uC-gsronu33B103d06b1
Method	BLASTX
NCBI GI	g2464901
BLAST score	211
E value	4.0e-17
Match length	86
% identity	47
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	237265
Seq. ID	uC-gsronu33B103d07b1
Method	BLASTX
NCBI GI	g2924515
BLAST score	243
E value	1.0e-20
Match length	108
% identity	44
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]
Seq. No.	237266
Seq. ID	uC-gsronu33B103e06b1
Method	BLASTX
NCBI GI	g4510347
BLAST score	428
E value	2.0e-42
Match length	117
% identity	69
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237267
Seq. ID	uC-gsronu33B103g01b1
Method	BLASTX
NCBI GI	g3033375
BLAST score	208
E value	1.0e-16
Match length	66
% identity	58
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
Seq. No.	237268
Seq. ID	uC-gsronu33B104a01b1
Method	BLASTX
NCBI GI	g124429
BLAST score	667
E value	3.0e-70

E value 1.0e-51
 Match length 152
 % identity 59
 NCBI Description (AC005917) putative senescence-associated protein 5
 [Arabidopsis thaliana]

Seq. No. 237274
 Seq. ID uC-gsronu33B104c11b1
 Method BLASTX
 NCBI GI g3292817
 BLAST score 433
 E value 7.0e-43
 Match length 128
 % identity 70
 NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237275
 Seq. ID uC-gsronu33B104d10b1
 Method BLASTX
 NCBI GI g2088648
 BLAST score 268
 E value 9.0e-24
 Match length 84
 % identity 65
 NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237276
 Seq. ID uC-gsronu33B104e05b1
 Method BLASTX
 NCBI GI g4262233
 BLAST score 233
 E value 1.0e-19
 Match length 98
 % identity 53
 NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237277
 Seq. ID uC-gsronu33B104e11b1
 Method BLASTX
 NCBI GI g4090259
 BLAST score 213
 E value 3.0e-17
 Match length 56
 % identity 66
 NCBI Description (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga
 menziesii]

Seq. No. 237278
 Seq. ID uC-gsronu33B104f04b1
 Method BLASTX
 NCBI GI g2586082
 BLAST score 238
 E value 1.0e-29
 Match length 156
 % identity 48
 NCBI Description (U72725) retrofit [Oryza longistaminata]

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Seq. No.	237279
Seq. ID	uC-gsronu33B104f05b1
Method	BLASTX
NCBI GI	g3776025
BLAST score	620
E value	9.0e-65
Match length	144
% identity	83
NCBI Description	(AJ010474) RNA helicase [Arabidopsis thaliana]
Seq. No.	237280
Seq. ID	uC-gsronu33B104f09b1
Method	BLASTX
NCBI GI	g1813891
BLAST score	152
E value	4.0e-10
Match length	38
% identity	87
NCBI Description	(Y10749) 1-aminocyclopropane-1-carboxylate oxidase [Betula pendula]
Seq. No.	237281
Seq. ID	uC-gsronu33B104h01b1
Method	BLASTX
NCBI GI	g1706282
BLAST score	355
E value	1.0e-33
Match length	101
% identity	64
NCBI Description	DISEASE RESISTANCE RESPONSE PROTEIN 206 >gi_508844 (U11716) disease resistance response protein 206-d [Pisum sativum]
Seq. No.	237282
Seq. ID	uC-gsronu33B106b08b2
Method	BLASTX
NCBI GI	g2760844
BLAST score	224
E value	3.0e-18
Match length	68
% identity	59
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237283
Seq. ID	uC-gsronu33B106b09b2
Method	BLASTX
NCBI GI	g2244996
BLAST score	572
E value	5.0e-59
Match length	136
% identity	79
NCBI Description	(Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]
Seq. No.	237284
Seq. ID	uC-gsronu33B106b12b2
Method	BLASTX
NCBI GI	g4432836

Seq. No. 237316
 Seq. ID uC-gsronu33B109d04b1
 Method BLASTX
 NCBI GI g3033375
 BLAST score 343
 E value 3.0e-32
 Match length 139
 % identity 50
 NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No. 237317
 Seq. ID uC-gsronu33B109e08b1
 Method BLASTX
 NCBI GI g4508079
 BLAST score 258
 E value 2.0e-22
 Match length 98
 % identity 50
 NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No. 237318
 Seq. ID uC-gsronu33B109e09b1
 Method BLASTX
 NCBI GI g1703200
 BLAST score 323
 E value 6.0e-30
 Match length 98
 % identity 66
 NCBI Description PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No. 237319
 Seq. ID uC-gsronu33B109f08b1
 Method BLASTX
 NCBI GI g4218187
 BLAST score 196
 E value 5.0e-15
 Match length 55
 % identity 40
 NCBI Description (AJ010165) leghemoglobin activating factor [Glycine max]

Seq. No. 237320
 Seq. ID uC-gsronu33B109g07b1
 Method BLASTX
 NCBI GI g3157933
 BLAST score 565
 E value 3.0e-58
 Match length 141
 % identity 69
 NCBI Description (AC002131) Contains similarity to box helicases gb_U29097 from C. elegans and to the ENBP1 gene product gb_X95995 from Vicia sativa. [Arabidopsis thaliana]

NCBI GI g3122367
 BLAST score 151
 E value 6.0e-10
 Match length 98
 % identity 36
 NCBI Description LIGATIN >gi_1377880 (U58337) ligatin [Mus musculus]

Seq. No. 237332
 Seq. ID uC-gsronu33B110h10b1
 Method BLASTX
 NCBI GI g951427
 BLAST score 434
 E value 5.0e-43
 Match length 109
 % identity 73
 NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]

Seq. No. 237333
 Seq. ID uC-gsronu33B111a07b1
 Method BLASTX
 NCBI GI g3549666
 BLAST score 144
 E value 4.0e-09
 Match length 40
 % identity 70
 NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 237334
 Seq. ID uC-gsronu33B111b03b1
 Method BLASTX
 NCBI GI g1345644
 BLAST score 439
 E value 1.0e-43
 Match length 116
 % identity 72
 NCBI Description CYTOCHROME P450 86A1 (CYPLXXXVI) >gi_940446_emb_CAA62082_ (X90458) cytochrome p450 [Arabidopsis thaliana]

Seq. No. 237335
 Seq. ID uC-gsronu33B111c04b1
 Method BLASTX
 NCBI GI g2344887
 BLAST score 207
 E value 2.0e-16
 Match length 57
 % identity 70
 NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 237336
 Seq. ID uC-gsronu33B111c09b1
 Method BLASTX
 NCBI GI g4206208
 BLAST score 231
 E value 4.0e-19
 Match length 97
 % identity 46

Seq. No. 237347
 Seq. ID uC-gsronu33B113c08b1
 Method BLASTX
 NCBI GI g1407705
 BLAST score 593
 E value 1.0e-61
 Match length 145
 % identity 75
 NCBI Description (U60202) lipoxygenase [Solanum tuberosum]

Seq. No. 237348
 Seq. ID uC-gsronu33B113c12b1
 Method BLASTX
 NCBI GI g3786012
 BLAST score 366
 E value 5.0e-35
 Match length 130
 % identity 52
 NCBI Description (AC005499) putative acid phosphatase [Arabidopsis thaliana]

Seq. No. 237349
 Seq. ID uC-gsronu33B113d10b1
 Method BLASTX
 NCBI GI g1086147
 BLAST score 331
 E value 6.0e-31
 Match length 80
 % identity 72
 NCBI Description protein S2 - Phalaris coerulescens >gi_556833_emb_CAA57520_ (X81992) S2 [Phalaris coerulescens]

Seq. No. 237350
 Seq. ID uC-gsronu33B113e01b1
 Method BLASTX
 NCBI GI g4539369
 BLAST score 290
 E value 3.0e-26
 Match length 85
 % identity 68
 NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 237351
 Seq. ID uC-gsronu33B113f01b1
 Method BLASTX
 NCBI GI g3757514
 BLAST score 408
 E value 6.0e-40
 Match length 80
 % identity 95
 NCBI Description (AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No. 237352
 Seq. ID uC-gsronu33B113f03b1
 Method BLASTX
 NCBI GI g417073
 BLAST score 518

Seq. ID uC-gsronu33B116a05b1
 Method BLASTX
 NCBI GI g1212759
 BLAST score 254
 E value 8.0e-22
 Match length 47
 % identity 89
 NCBI Description (X89192) DNA binding protein [Arabidopsis thaliana]

Seq. No. 237369
 Seq. ID uC-gsronu33B116a06b1
 Method BLASTX
 NCBI GI g4455293
 BLAST score 359
 E value 4.0e-34
 Match length 133
 % identity 60
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 237370
 Seq. ID uC-gsronu33B116b08b1
 Method BLASTX
 NCBI GI g3395441
 BLAST score 247
 E value 4.0e-21
 Match length 65
 % identity 68
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 237371
 Seq. ID uC-gsronu33B116c01b1
 Method BLASTX
 NCBI GI g1001649
 BLAST score 229
 E value 5.0e-19
 Match length 116
 % identity 47
 NCBI Description (D64002) DNA gyrase A subunit [Synechocystis sp.]

Seq. No. 237372
 Seq. ID uC-gsronu33B116c04b1
 Method BLASTX
 NCBI GI g336392
 BLAST score 271
 E value 7.0e-24
 Match length 89
 % identity 66
 NCBI Description (J05215) ribosomal protein S17 [Arabidopsis thaliana]

Seq. No. 237373
 Seq. ID uC-gsronu33B116c05b1
 Method BLASTX
 NCBI GI g4455330
 BLAST score 323
 E value 6.0e-30
 Match length 149
 % identity 46

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Seq. No. 237379
 Seq. ID uC-gsronu33B116g03b1
 Method BLASTX
 NCBI GI g3176072
 BLAST score 133
 E value 4.0e-16
 Match length 52
 % identity 88
 NCBI Description (AJ002485) protein phosphatase 1, catalytic beta subunit [Medicago sativa]

Seq. No. 237380
 Seq. ID uC-gsronu33B116g04b1
 Method BLASTX
 NCBI GI g3786011
 BLAST score 678
 E value 2.0e-71
 Match length 149
 % identity 85
 NCBI Description (AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No. 237381
 Seq. ID uC-gsronu33B116h01b1
 Method BLASTX
 NCBI GI g2809262
 BLAST score 257
 E value 2.0e-22
 Match length 109
 % identity 46
 NCBI Description (AC002560) F21B7.31 [Arabidopsis thaliana]

Seq. No. 237382
 Seq. ID uC-gsronu33B117a07b1
 Method BLASTX
 NCBI GI g3831471
 BLAST score 178
 E value 4.0e-13
 Match length 57
 % identity 56
 NCBI Description (AC005700) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237383
 Seq. ID uC-gsronu33B117a10b1
 Method BLASTX
 NCBI GI g3818624
 BLAST score 765
 E value 1.0e-81
 Match length 154
 % identity 96
 NCBI Description (AF095912) actin related protein 2; ARP2 [Arabidopsis thaliana]

Seq. No. 237384
 Seq. ID uC-gsronu33B117c04b1

ribosomal protein S8 [Oryza sativa]

Seq. No. 237390
 Seq. ID uC-gsronu33B117h03b1
 Method BLASTX
 NCBI GI g2443836
 BLAST score 206
 E value 2.0e-16
 Match length 57
 % identity 60
 NCBI Description (AF020793) tonoplast intrinsic protein homolog MSMCP1 [Medicago sativa]

Seq. No. 237391
 Seq. ID uC-gsronu33B121h01b1
 Method BLASTX
 NCBI GI g3914449
 BLAST score 336
 E value 7.0e-32
 Match length 72
 % identity 89
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]

Seq. No. 237392
 Seq. ID uC-gsronu33B124a03b1
 Method BLASTX
 NCBI GI g1279640
 BLAST score 452
 E value 5.0e-45
 Match length 134
 % identity 62
 NCBI Description (X92204) NAM [Petunia x hybrida]

Seq. No. 237393
 Seq. ID uC-gsronu33B124a06b1
 Method BLASTX
 NCBI GI g3935183
 BLAST score 249
 E value 2.0e-21
 Match length 113
 % identity 49
 NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]

Seq. No. 237394
 Seq. ID uC-gsronu33B124b01b1
 Method BLASTX
 NCBI GI g3540181
 BLAST score 230
 E value 5.0e-19
 Match length 123
 % identity 46
 NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 237395
 Seq. ID uC-gsronu33B124b11b1

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 237416

Seq. ID uC-gsronu33B126b01b1

Method BLASTX

NCBI GI g1174592

BLAST score 535

E value 5.0e-55

Match length 103

% identity 97

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
- garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
sativum]

Seq. No. 237417

Seq. ID uC-gsronu33B126b11b1

Method BLASTX

NCBI GI g4455338

BLAST score 538

E value 3.0e-55

Match length 114

% identity 91

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 237418

Seq. ID uC-gsronu33B126c09b1

Method BLASTX

NCBI GI g3269287

BLAST score 344

E value 1.0e-32

Match length 85

% identity 79

NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No. 237419

Seq. ID uC-gsronu33B126d08b1

Method BLASTX

NCBI GI g3249068

BLAST score 263

E value 9.0e-23

Match length 128

% identity 42

NCBI Description (AC004473) Contains similarity to zinc-binding protein
(PWA33) gb_L04190 from Pleurodeles waltlii. [Arabidopsis
thaliana]

Seq. No. 237420

Seq. ID uC-gsronu33B126d09b1

Method BLASTX

NCBI GI g1420887

BLAST score 189

E value 3.0e-14

Match length 69

% identity 48

NCBI Description (U34334) non-specific lipid transfer-like protein
[Phaseolus vulgaris]

09684016.101000

Seq. No. 237421
 Seq. ID uC-gsronu33B126e02b1
 Method BLASTX
 NCBI GI g4510346
 BLAST score 147
 E value 6.0e-10
 Match length 40
 % identity 68
 NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237422
 Seq. ID uC-gsronu33B126e06b1
 Method BLASTX
 NCBI GI g1173223
 BLAST score 171
 E value 2.0e-12
 Match length 36
 % identity 94
 NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_454848 (L28831) ribosomal protein S11 [Glycine max]

Seq. No. 237423
 Seq. ID uC-gsronu33B126f04b1
 Method BLASTX
 NCBI GI g4378848
 BLAST score 415
 E value 1.0e-40
 Match length 139
 % identity 56
 NCBI Description (AF124349) hydrolase [Zymomonas mobilis]

Seq. No. 237424
 Seq. ID uC-gsronu33B126f10b1
 Method BLASTX
 NCBI GI g3478637
 BLAST score 282
 E value 3.0e-25
 Match length 123
 % identity 41
 NCBI Description (AC005546) R29425_1 [Homo sapiens]

Seq. No. 237425
 Seq. ID uC-gsronu33B126g06b1
 Method BLASTX
 NCBI GI g3885334
 BLAST score 209
 E value 6.0e-28
 Match length 121
 % identity 65
 NCBI Description (AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No. 237426
 Seq. ID uC-gsronu33B126h09b1
 Method BLASTX
 NCBI GI g283503
 BLAST score 138

E value 8.0e-09
 Match length 43
 % identity 70
 NCBI Description tubulin alpha chain - Euplotes vannus (SGC9)
 >gi_9327_emb_CAA77816_ (Z11769) alpha-Tubulin [Euplotes
 vannus]

Seq. No. 237427
 Seq. ID uC-gsronu33B127a01b1
 Method BLASTX
 NCBI GI g2252866
 BLAST score 308
 E value 3.0e-28
 Match length 88
 % identity 80
 NCBI Description (AF013294) contains region of similarity to SYT
 [Arabidopsis thaliana]

Seq. No. 237428
 Seq. ID uC-gsronu33B127a03b1
 Method BLASTX
 NCBI GI g4455207
 BLAST score 270
 E value 3.0e-30
 Match length 88
 % identity 82
 NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 237429
 Seq. ID uC-gsronu33B127a06b1
 Method BLASTX
 NCBI GI g2443887
 BLAST score 222
 E value 2.0e-18
 Match length 61
 % identity 74
 NCBI Description (AC002294) Similar to transcription factor
 gb_Z46606_1658307 and others [Arabidopsis thaliana]

Seq. No. 237430
 Seq. ID uC-gsronu33B127a07b1
 Method BLASTX
 NCBI GI g130771
 BLAST score 173
 E value 2.0e-12
 Match length 82
 % identity 41
 NCBI Description PHOSPHATIDYLINOSITOL TRANSFER PROTEIN ALPHA ISOFORM (PTDINS
 TRANSFER PROTEIN ALPHA) (PTDINSTP) (PI-TP-ALPHA)
 >gi_92602_pir_A34391 phosphatidylinositol transfer protein
 - rat >gi_206495 (M25758) phosphatidylinositol transfer
 protein [Rattus norvegicus]

Seq. No. 237431
 Seq. ID uC-gsronu33B127a08b1
 Method BLASTX
 NCBI GI g2662343

Method	BLASTX
NCBI GI	g4467158
BLAST score	293
E value	2.0e-26
Match length	148
% identity	50
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]
Seq. No.	237442
Seq. ID	uC-gsronu33B129g05b1
Method	BLASTX
NCBI GI	g1805254
BLAST score	409
E value	5.0e-40
Match length	89
% identity	83
NCBI Description	(U62622) monogalactosyldiacylglycerol synthase [Cucumis sativus]
Seq. No.	237443
Seq. ID	uC-gsronu33B129g09b1
Method	BLASTX
NCBI GI	g1352442
BLAST score	307
E value	6.0e-28
Match length	75
% identity	75
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_1002917 (U34598) p28 [Oryza sativa]
Seq. No.	237444
Seq. ID	uC-gsronu33B129h05b1
Method	BLASTX
NCBI GI	g4545262
BLAST score	215
E value	3.0e-17
Match length	48
% identity	85
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]
Seq. No.	237445
Seq. ID	uC-gsronu33B129h06b1
Method	BLASTX
NCBI GI	g4454484
BLAST score	383
E value	8.0e-37
Match length	120
% identity	62
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.	237446
Seq. ID	uC-gsronu33B130e03b1
Method	BLASTX

E value 6.0e-30
 Match length 63
 % identity 97
 NCBI Description CHALCONE SYNTHASE 3 (NARINGENIN-CHALCONE SYNTHASE 3)
 >gi_1084446_pir_S55464 chalcone synthase 3 - gerbera
 hybrid >gi_1362143_pir_S56701 chalcone synthase 3 -
 gerbera hybrid >gi_853932_emb_CAA86220_ (Z38098) chalcone
 synthase [Gerbera hybrida]

Seq. No. 237452
 Seq. ID uC-gsronu33B130f10b1
 Method BLASTX
 NCBI GI g4249388
 BLAST score 326
 E value 2.0e-30
 Match length 87
 % identity 71
 NCBI Description (AC005966) Similar to gb_AF025438 Opa-interacting protein
 (OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 237453
 Seq. ID uC-gsronu33B130h04b1
 Method BLASTX
 NCBI GI g2191175
 BLAST score 266
 E value 2.0e-23
 Match length 113
 % identity 50
 NCBI Description (AF007270) A_IG002R16.24 gene product [Arabidopsis
 thaliana]

Seq. No. 237454
 Seq. ID uC-gsronu33B130h10b1
 Method BLASTX
 NCBI GI g3738297
 BLAST score 156
 E value 6.0e-11
 Match length 43
 % identity 13
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 237455
 Seq. ID uC-gsronu33B132a08b1
 Method BLASTX
 NCBI GI g3661610
 BLAST score 138
 E value 7.0e-09
 Match length 60
 % identity 43
 NCBI Description (AF092565) splicing factor Prp8 [Homo sapiens]

Seq. No. 237456
 Seq. ID uC-gsronu33B132b09b1
 Method BLASTX
 NCBI GI g100226
 BLAST score 182
 E value 3.0e-16

Match length 142
 % identity 39
 NCBI Description hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf_1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No. 237457
 Seq. ID uC-gsronu33B132b10b1
 Method BLASTX
 NCBI GI g4455159
 BLAST score 337
 E value 7.0e-32
 Match length 95
 % identity 64
 NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 237458
 Seq. ID uC-gsronu33B132e02b1
 Method BLASTX
 NCBI GI g3128203
 BLAST score 488
 E value 3.0e-49
 Match length 138
 % identity 68
 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 237459
 Seq. ID uC-gsronu33B132f06b1
 Method BLASTX
 NCBI GI g1351279
 BLAST score 497
 E value 2.0e-50
 Match length 116
 % identity 84
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase [Petunia x hybrida]

Seq. No. 237460
 Seq. ID uC-gsronu33B132f12b1
 Method BLASTX
 NCBI GI g3738285
 BLAST score 301
 E value 2.0e-27
 Match length 64
 % identity 83
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 237461
 Seq. ID uC-gsronu33B132g02b1
 Method BLASTX
 NCBI GI g4567226
 BLAST score 183
 E value 2.0e-13
 Match length 73
 % identity 55

Method BLASTX
 NCBI GI g1777443
 BLAST score 407
 E value 8.0e-40
 Match length 91
 % identity 85
 NCBI Description (U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310)
 DNA-binding protein CCA1 [Arabidopsis thaliana] >gi_4090569
 (U79156) CCA1 [Arabidopsis thaliana]

Seq. No. 237468
 Seq. ID uC-gsronu33B134c03b1
 Method BLASTX
 NCBI GI g3461835
 BLAST score 502
 E value 5.0e-51
 Match length 123
 % identity 79
 NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]
 >gi_3927840 (AC005727) putative protein kinase [Arabidopsis
 thaliana]

Seq. No. 237469
 Seq. ID uC-gsronu33B134d09b1
 Method BLASTX
 NCBI GI g266989
 BLAST score 289
 E value 5.0e-26
 Match length 93
 % identity 62
 NCBI Description GTP-BINDING PROTEIN SAR1B >gi_322517_pir_S28603
 GTP-binding protein - Arabidopsis thaliana >gi_166734
 (M95795) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 237470
 Seq. ID uC-gsronu33B134e05b1
 Method BLASTX
 NCBI GI g3395756
 BLAST score 168
 E value 3.0e-18
 Match length 91
 % identity 56
 NCBI Description (U76297) plantacyanin [Arabidopsis thaliana] >gi_3461812
 (AC004138) putative basic blue protein [Arabidopsis
 thaliana]

Seq. No. 237471
 Seq. ID uC-gsronu33B134e08b1
 Method BLASTX
 NCBI GI g3702343
 BLAST score 271
 E value 5.0e-24
 Match length 114
 % identity 53
 NCBI Description (AC005397) putative homeotic gene regulator [Arabidopsis
 thaliana]

Method BLASTX
 NCBI GI g2281090
 BLAST score 458
 E value 7.0e-46
 Match length 132
 % identity 70
 NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237478
 Seq. ID uC-gsronu33B136d06b1
 Method BLASTX
 NCBI GI g4006896
 BLAST score 280
 E value 4.0e-25
 Match length 113
 % identity 60
 NCBI Description (Z99708) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 237479
 Seq. ID uC-gsronu33B136e12b1
 Method BLASTX
 NCBI GI g2760839
 BLAST score 333
 E value 4.0e-31
 Match length 134
 % identity 51
 NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 237480
 Seq. ID uC-gsronu33B136f02b1
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 7.0e-15
 Match length 47
 % identity 68
 NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No. 237481
 Seq. ID uC-gsronu33B136f04b1
 Method BLASTX
 NCBI GI g2911799
 BLAST score 494
 E value 6.0e-50
 Match length 121
 % identity 83
 NCBI Description (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No. 237482
 Seq. ID uC-gsronu33B136f09b1
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 2.0e-14
 Match length 47

NCBI Description (X95269) LRR protein [*Lycopersicon esculentum*]

Seq. No. 237488
Seq. ID uC-gsronu33B137a06b1
Method BLASTX
NCBI GI g2781345
BLAST score 507
E value 2.0e-51
Match length 149
% identity 62

NCBI Description (AC003113) F24O1.2 [*Arabidopsis thaliana*]

Seq. No. 237489
Seq. ID uC-gsronu33B137b02b1
Method BLASTX
NCBI GI g2995405
BLAST score 268
E value 2.0e-23
Match length 75
% identity 65

NCBI Description (Y12432) polyprotein [*Ananas comosus*]

Seq. No. 237490
Seq. ID uC-gsronu33B137b08b1
Method BLASTX
NCBI GI g3183640
BLAST score 191
E value 9.0e-15
Match length 35
% identity 97

NCBI Description (AJ005869) transmembrane channel protein [*Cicer arietinum*]

Seq. No. 237491
Seq. ID uC-gsronu33B137c06b1
Method BLASTX
NCBI GI g3292823
BLAST score 175
E value 1.0e-12
Match length 105
% identity 36

NCBI Description (AL031018) putative protein [*Arabidopsis thaliana*]

Seq. No. 237492
Seq. ID uC-gsronu33B137c07b1
Method BLASTX
NCBI GI g1840045
BLAST score 148
E value 2.0e-09
Match length 153
% identity 28

NCBI Description (U49082) transporter protein [*Homo sapiens*]

Seq. No. 237493
Seq. ID uC-gsronu33B137c08b1
Method BLASTX
NCBI GI g4538920
BLAST score 275

E value 3.0e-24
 Match length 76
 % identity 38
 NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No. 237494
 Seq. ID uC-gsronu33B137e04b1
 Method BLASTX
 NCBI GI g3643602
 BLAST score 399
 E value 9.0e-39
 Match length 133
 % identity 62
 NCBI Description (AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No. 237495
 Seq. ID uC-gsronu33B137e10b1
 Method BLASTX
 NCBI GI g3894157
 BLAST score 366
 E value 6.0e-35
 Match length 158
 % identity 8
 NCBI Description (AC005312) putative protein kinase, 3' partial [Arabidopsis thaliana]

Seq. No. 237496
 Seq. ID uC-gsronu33B137e11b1
 Method BLASTX
 NCBI GI g115607
 BLAST score 452
 E value 5.0e-45
 Match length 156
 % identity 54
 NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) (PEPC)
 >gi_68033_pir_QYEC phosphoenolpyruvate carboxylase (EC 4.1.1.31) - Escherichia coli >gi_4558284_pdb_1FIY_Three-Dimensional Structure Of Phosphoenolpyruvate Carboxylase From Escherichia Coli At 2.8 A Resolution.
 >gi_48666_emb_CAA29332_(X05903) PEP carboxylase (AA 1-883) [Escherichia coli] >gi_396303 (U00006) phosphoenolpyruvate carboxylase [Escherichia coli] >gi_1790393 (AE000469) phosphoenolpyruvate carboxylase [Escherichia coli] >gi_352091_prf_1005219A carboxylase,phosphoenolpyruvate [Escherichia coli]

Seq. No. 237497
 Seq. ID uC-gsronu33B137f04b1
 Method BLASTX
 NCBI GI g2789660
 BLAST score 334
 E value 3.0e-31
 Match length 137
 % identity 56
 NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No.	237498
Seq. ID	uC-gsronu33B137g05b1
Method	BLASTX
NCBI GI	g3024017
BLAST score	326
E value	2.0e-30
Match length	79
% identity	85
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]
Seq. No.	237499
Seq. ID	uC-gsronu33B137g08b1
Method	BLASTX
NCBI GI	g2980790
BLAST score	144
E value	3.0e-09
Match length	43
% identity	56
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237500
Seq. ID	uC-gsronu33B137g11b1
Method	BLASTX
NCBI GI	g3258571
BLAST score	522
E value	3.0e-53
Match length	139
% identity	79
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	237501
Seq. ID	uC-gsronu33B137h11b1
Method	BLASTX
NCBI GI	g1332579
BLAST score	709
E value	4.0e-75
Match length	143
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]
Seq. No.	237502
Seq. ID	uC-gsronu33B138a02b1
Method	BLASTX
NCBI GI	g3264611
BLAST score	254
E value	7.0e-22
Match length	52
% identity	90
NCBI Description	(AF061511) seven in absentia homolog [Zea mays]
Seq. No.	237503
Seq. ID	uC-gsronu33B138a03b1
Method	BLASTX
NCBI GI	g1514649

BLAST score 345
 E value 2.0e-32
 Match length 154
 % identity 49
 NCBI Description (X86021) potassium channel [Solanum tuberosum]

Seq. No. 237504
 Seq. ID uC-gsronu33B138b02b1
 Method BLASTX
 NCBI GI g3193316
 BLAST score 569
 E value 8.0e-59
 Match length 140
 % identity 80
 NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 237505
 Seq. ID uC-gsronu33B138b06b1
 Method BLASTX
 NCBI GI g2462753
 BLAST score 391
 E value 3.0e-38
 Match length 82
 % identity 83
 NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 237506
 Seq. ID uC-gsronu33B138b11b1
 Method BLASTX
 NCBI GI g2088648
 BLAST score 191
 E value 8.0e-15
 Match length 80
 % identity 50
 NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237507
 Seq. ID uC-gsronu33B138e05b1
 Method BLASTX
 NCBI GI g2982331
 BLAST score 316
 E value 3.0e-29
 Match length 64
 % identity 98
 NCBI Description (AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No. 237508
 Seq. ID uC-gsronu33B138f04b1
 Method BLASTX
 NCBI GI g2827002
 BLAST score 255
 E value 3.0e-22
 Match length 51
 % identity 100
 NCBI Description (AF005993) HSP70 [Triticum aestivum]

Seq. No.	237519
Seq. ID	uC-gsronu33B139c10b1
Method	BLASTX
NCBI GI	g3121739
BLAST score	311
E value	2.0e-28
Match length	144
% identity	16
NCBI Description	ANGIO-ASSOCIATED MIGRATORY CELL PROTEIN >gi_2134759_pir_I39383 angio-associated migratory cell protein - human >gi_870803 (M95627) angio-associated migratory cell protein [Homo sapiens] >gi_4557229_ref_NP_001078.1_pAAMP_ angio-associated, migratory cell protein
Seq. No.	237520
Seq. ID	uC-gsronu33B139c11b1
Method	BLASTX
NCBI GI	g2702272
BLAST score	197
E value	3.0e-15
Match length	69
% identity	17
NCBI Description	(AC003033) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237521
Seq. ID	uC-gsronu33B139d06b1
Method	BLASTX
NCBI GI	g3738327
BLAST score	292
E value	2.0e-26
Match length	97
% identity	65
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]
Seq. No.	237522
Seq. ID	uC-gsronu33B139e08b1
Method	BLASTX
NCBI GI	g3201680
BLAST score	499
E value	1.0e-50
Match length	140
% identity	67
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]
Seq. No.	237523
Seq. ID	uC-gsronu33B139f12b1
Method	BLASTX
NCBI GI	g4538929
BLAST score	394
E value	3.0e-38
Match length	155
% identity	59
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No. 237524
 Seq. ID uC-gsronu33B139g10b1
 Method BLASTX
 NCBI GI g585338
 BLAST score 224
 E value 2.0e-18
 Match length 54
 % identity 81
 NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
 >gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza sativa]

Seq. No. 237525
 Seq. ID uC-gsronu33B141a06b1
 Method BLASTX
 NCBI GI g3023816
 BLAST score 284
 E value 2.0e-25
 Match length 56
 % identity 96
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No. 237526
 Seq. ID uC-gsronu33B141b06b1
 Method BLASTX
 NCBI GI g4056506
 BLAST score 219
 E value 1.0e-17
 Match length 135
 % identity 34
 NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 237527
 Seq. ID uC-gsronu33B141b09b1
 Method BLASTX
 NCBI GI g2832642
 BLAST score 171
 E value 4.0e-12
 Match length 137
 % identity 19
 NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 237528
 Seq. ID uC-gsronu33B141d12b1
 Method BLASTX
 NCBI GI g1706958
 BLAST score 733
 E value 6.0e-78
 Match length 154
 % identity 90
 NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 237529
 Seq. ID uC-gsronu33B141e05b1

Method BLASTX
 NCBI GI g81857
 BLAST score 340
 E value 7.0e-32
 Match length 71
 % identity 90
 NCBI Description IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]

Seq. No. 237535
 Seq. ID uC-gsronu33B143a12b1
 Method BLASTX
 NCBI GI g4454043
 BLAST score 499
 E value 1.0e-50
 Match length 151
 % identity 64
 NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 237536
 Seq. ID uC-gsronu33B143c03b1
 Method BLASTX
 NCBI GI g3426039
 BLAST score 447
 E value 1.0e-44
 Match length 126
 % identity 66
 NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 237537
 Seq. ID uC-gsronu33B143c06b1
 Method BLASTX
 NCBI GI g3643607
 BLAST score 326
 E value 1.0e-30
 Match length 83
 % identity 40
 NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 237538
 Seq. ID uC-gsronu33B143c07b1
 Method BLASTX
 NCBI GI g2191165
 BLAST score 209
 E value 1.0e-16
 Match length 82
 % identity 50
 NCBI Description (AF007270) A_IG002P16.14 gene product [Arabidopsis thaliana]

Seq. No. 237539
 Seq. ID uC-gsronu33B143d02b1
 Method BLASTX
 NCBI GI g3548801
 BLAST score 188
 E value 2.0e-14

Match length 129
 % identity 50
 NCBI Description (U54558) translation initiation factor eIF3 p66 subunit
 [Homo sapiens] >gi_4200328_emb_CAA18440_ (AL022313)
 EIF3-P66 [Homo sapiens]
 >gi_4503523_ref_NP_003744.1_pEIF3S7_ UNKNOWN

Seq. No. 237550
 Seq. ID uC-gsronu33B144f09b1
 Method BLASTX
 NCBI GI g2980777
 BLAST score 217
 E value 1.0e-17
 Match length 110
 % identity 41
 NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 237551
 Seq. ID uC-gsronu33B144h03b1
 Method BLASTX
 NCBI GI g2970051
 BLAST score 243
 E value 1.0e-20
 Match length 75
 % identity 63
 NCBI Description (AB012110) ARG10 [Vigna radiata]

Seq. No. 237552
 Seq. ID uC-gsronu33B145c08b1
 Method BLASTX
 NCBI GI g3687223
 BLAST score 160
 E value 8.0e-11
 Match length 38
 % identity 82
 NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237553
 Seq. ID uC-gsronu33B145d10b1
 Method BLASTX
 NCBI GI g548770
 BLAST score 213
 E value 1.0e-28
 Match length 81
 % identity 83
 NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal
 protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
 ribosomal protein L3 [Oryza sativa]

Seq. No. 237554
 Seq. ID uC-gsronu33B145f08b1
 Method BLASTX
 NCBI GI g3046693
 BLAST score 308
 E value 3.0e-28
 Match length 91
 % identity 60

NCBI GI g2827528
 BLAST score 155
 E value 2.0e-10
 Match length 43
 % identity 89
 NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 237566
 Seq. ID uC-gsronu33B146g07b1
 Method BLASTX
 NCBI GI g4220462
 BLAST score 356
 E value 7.0e-34
 Match length 124
 % identity 54
 NCBI Description (AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No. 237567
 Seq. ID uC-gsronu33B146h01b1
 Method BLASTX
 NCBI GI g4539305
 BLAST score 223
 E value 2.0e-18
 Match length 42
 % identity 88
 NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 237568
 Seq. ID uC-gsronu33B147a01b1
 Method BLASTX
 NCBI GI g2351374
 BLAST score 326
 E value 6.0e-31
 Match length 70
 % identity 91
 NCBI Description (U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No. 237569
 Seq. ID uC-gsronu33B147b02b1
 Method BLASTX
 NCBI GI g3879754
 BLAST score 214
 E value 5.0e-17
 Match length 108
 % identity 41
 NCBI Description (Z72514) Similarity to Rabbit glycogenin (SW:GLYG_RABIT) [Caenorhabditis elegans]

Seq. No. 237570
 Seq. ID uC-gsronu33B147c05b1
 Method BLASTX
 NCBI GI g4185819
 BLAST score 180
 E value 3.0e-13

from this gene. [Arabidopsis thaliana]

Seq. No. 237581
Seq. ID uC-gsronu33B149a05b1
Method BLASTX
NCBI GI g4185819
BLAST score 192
E value 1.0e-14
Match length 47
% identity 68
NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No. 237582
Seq. ID uC-gsronu33B149a06b1
Method BLASTX
NCBI GI g3927835
BLAST score 559
E value 1.0e-57
Match length 132
% identity 80
NCBI Description (AC005727) similar to Streptomyces PapA [Arabidopsis thaliana]

Seq. No. 237583
Seq. ID uC-gsronu33B149c12b1
Method BLASTX
NCBI GI g218157
BLAST score 191
E value 1.0e-14
Match length 43
% identity 86
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No. 237584
Seq. ID uC-gsronu33B149e05b1
Method BLASTX
NCBI GI g1703446
BLAST score 449
E value 9.0e-45
Match length 122
% identity 70
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
>gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
>gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No. 237585
Seq. ID uC-gsronu33B149f10b1
Method BLASTX
NCBI GI g2541876
BLAST score 279
E value 1.0e-24
Match length 150
% identity 39
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No. 237586
 Seq. ID uC-gsronu33B149g08b1
 Method BLASTX
 NCBI GI g4056496
 BLAST score 516
 E value 1.0e-52
 Match length 119
 % identity 75
 NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 237587
 Seq. ID uC-gsronu33B149g11b1
 Method BLASTX
 NCBI GI g2827141
 BLAST score 340
 E value 3.0e-32
 Match length 65
 % identity 91
 NCBI Description (AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 237588
 Seq. ID uC-gsronu33B149h01b1
 Method BLASTX
 NCBI GI g4512705
 BLAST score 476
 E value 4.0e-48
 Match length 105
 % identity 89
 NCBI Description (AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 237589
 Seq. ID uC-gsronu33B149h07b1
 Method BLASTX
 NCBI GI g4432855
 BLAST score 234
 E value 1.0e-19
 Match length 116
 % identity 53
 NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 237590
 Seq. ID uC-gsronu33B150a11b1
 Method BLASTX
 NCBI GI g2129770
 BLAST score 183
 E value 1.0e-13
 Match length 48
 % identity 65
 NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 237591
 Seq. ID uC-gsronu33B150d06b1
 Method BLASTX
 NCBI GI g1174867
 BLAST score 153
 E value 3.0e-10
 Match length 35
 % identity 83
 NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862_(X79275)
 ubiquinol--cytochrome c reductase [Solanum tuberosum]
 >gi_1094912_prf_2107179A cytochrome c oxidase:SUBUNIT=8.2kd [Solanum tuberosum]

Seq. No. 237592
 Seq. ID uC-gsronu33B150d10b1
 Method BLASTX
 NCBI GI g3335366
 BLAST score 218
 E value 2.0e-17
 Match length 76
 % identity 54
 NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 237593
 Seq. ID uC-gsronu33B150d12b1
 Method BLASTX
 NCBI GI g3643082
 BLAST score 149
 E value 1.0e-09
 Match length 67
 % identity 51
 NCBI Description (AF075579) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No. 237594
 Seq. ID uC-gsronu33B150e01b1
 Method BLASTX
 NCBI GI g3582434
 BLAST score 255
 E value 4.0e-22
 Match length 97
 % identity 58
 NCBI Description (AB017273) low-molecular-weight heat shock protein [Cuscuta japonica]

Seq. No. 237595
 Seq. ID uC-gsronu33B150g10b1
 Method BLASTX
 NCBI GI g4455293
 BLAST score 253
 E value 1.0e-21
 Match length 58
 % identity 86
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]